Welcome to Biology 1B!

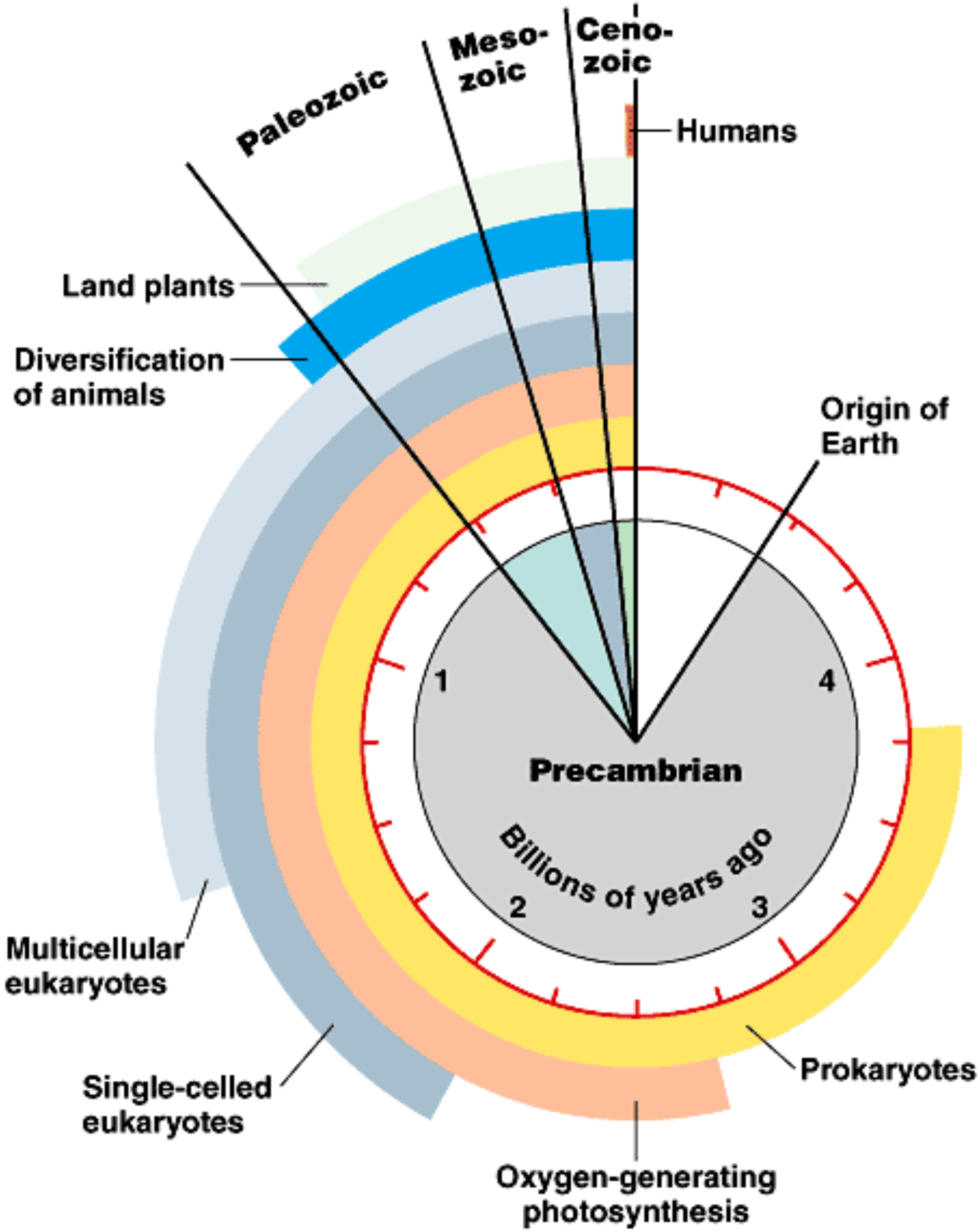
The Origin and History of Life on Earth

Key Topics:

- **1. Hypotheses for the Origin of Life on Earth**
- **2. The Fossil Record**
- **3. History of Life on Earth**

Origin of Life on Earth

- 13.7 bya – Universe began with the Big Bang
- 4.6 bya -- Our solar system began
- The Earth is ~ 4.55 billion years old
- 4 bya – Earth had cooled enough for outer layers to solidify and oceans to form
- between 4 and 3.5 bya – Life began (bacterial)
- UC Museum of Paleontology



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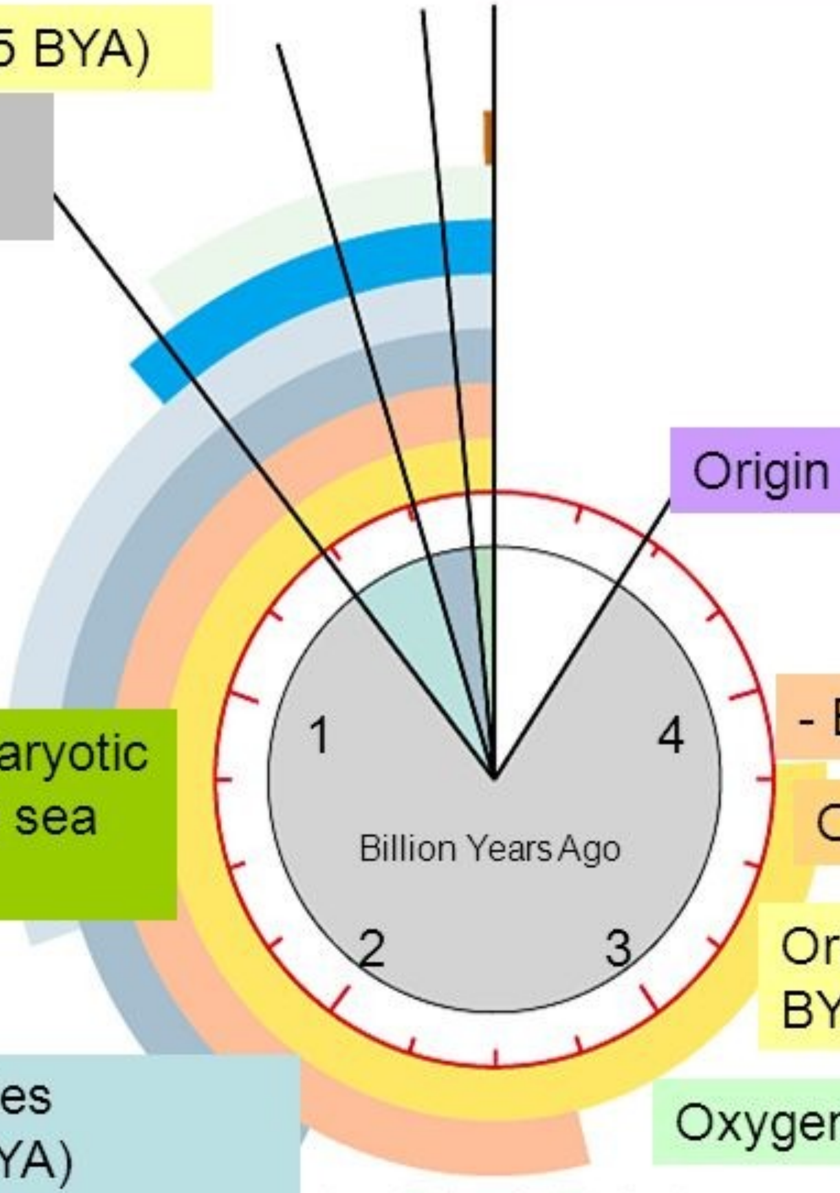
History of Earth on a clock…



Dinosaurs (.1 BYA)

Humans (Today)

Colonization of Land (.5 BYA)

Marine invertebrates evolve (.54 BYA)

Origin of Earth (4.5 BYA)

- Earth Cools(3.9 BYA)

Multicellular eukaryotic life begins in the sea (1.2 BYA)

Origin of life (3.8 BYA)

Origin of Prokaryotes (3.5 BYA)

Endosymbiosis creates eukaryotic life (2.1 BYA)

Oxygen in atmosphere (2.7 BYA)

A Brief Look at Earth's History

The biological, geological, and climatic events listed appear in reverse chronological order, with the oldest event (at the bottom) and the most recent event (at the top).

Era	Period	Epoch	Beginning of Interval	Major Biological Events of the Era	Major Geologic and Climatic Events of the Era
Cenozoic	**Quaternary**	**Holocene or Recent**	(10,000 years ago)	Human Civilization	Earth's climate has been stable for the past 8,000 years. Great Lakes formed as glacial ice melted. The peak of the last ice age was 21,000 years ago. Earth experienced several periods of glacial conditions (ice ages) and interglacial conditions. ----------------------------------
		Pleistocene	1.7 million years ago (MYA)	Saber-toothed Cats, First Humans, Bears, Mammoths, Sloths	
	Tertiary	**Pliocene** **Miocene** **Oligocene** **Eocene** **Paleocene**	66 MYA	Flowering Plants Horses, Cats, Dogs, Primates, Camels, Rhinoceroses, Deer, Pigs, Small Mammals	Earth became colder and drier. Volcanic activity increased in western North America. Andes, Alps, and Himalaya Mountains formed as crustal plates moved. Colorado River carved out Grand Canyon. Inland seas in North America drained away.
Mesozoic	**Cretaceous**			Extinction of Dinosaurs First Flowering Plants Most Dinosaurs	Asteroid impact likely caused extinction of dinosaurs. Rocky and Sierra Nevada Mountains formed. Climate was much warmer than today. Shallow seas covered much of North America. Atlantic Ocean formed. North America and Africa moved apart. Pangaea began to break up.
	Jurassic			Larger, Fiercer Dinosaurs First Birds First Small Mammals	
	Triassic		245 MYA	Many Cycads and Conifer Trees Reptiles First Dinosaurs	
Paleozoic	**Permian**			Many Amphibians and Reptiles First Conifer Plants	Land became drier. Basins were larger so water drained into them. Ural and Appalachian Mountains formed. Continents moved together, forming Pangaea. Coal formed in swampy regions. Shallow seas covered most of land.
	Carboniferous Pennsylvanian Mississippian			First Reptiles Coal Forming Swamps	
	Devonian			First Amphibians, Sharks and Insects	
	Silurian			Coral Reefs Form First Land Plants	
	Ordovician			First Fish (Vertebrates)	
	Cambrian		570 MYA	First Invertebrates; Trilobites, Brachiopods	
Precambrian			4.6 billion years ago	Simple Marine Life, Bacteria, Algae, Jellyfish	Ozone layer formed. Outgassing caused the atmosphere to form and eventually the oceans. Meteorites bombarded Earth. Solid Earth divided into core, mantle, crust. Earth formed approximately 4.6 billion years ago.

M.Y.A. = million years ago

Origin of life –
four overlapping stages

1. **Nucleotides** and **amino acids** produced prior to the existence of cells (building blocks)

2. Nucleotides and amino acids became polymerized to form **DNA**, **RNA** and **proteins** (chains of building blocks)

3. Polymers became enclosed in **membranes** (package it)

4. Polymers enclosed in membranes acquired **cellular properties** (functional packages)

Understanding Evolution UC Berkeley link

Stage 1: Origin of organic molecules

- Conditions on primitive Earth may have been conducive to **formation** of organic molecules

- Prebiotic or **abiotic synthesis** (https://en.wikipedia.org/wiki/Abiogenesis)
  - Little free oxygen gas (so little oxidation)
  - No living organisms (so molecules not eaten)
  - Molecules slowly accumulated
  - Formed prebiotic soup (Oparin/Haldane hypoth.)

There are **several hypotheses** on where and how organic molecules originated

A. Reducing atmosphere hypothesis

- ❑Based on geological data
- ❑Atmosphere rich in water vapor, H_2, CH_4, NH_3 (and little O_2) = reducing environment (CH_4 & NH_3 give up electrons to other molecules, reducing them)
- ❑**Stanley Miller & Harold Urey** used a chamber apparatus to simulate this atmosphere and bolts of lightning in 1953 (https://en.wikipedia.org/wiki/Stanley_Miller)
- ❑Formed precursors of complex organic molecules, which combined into amino acids. Later sugars and nitrogenous bases
- ❑First attempt to apply scientific experiments to understand origin of organic compounds and life

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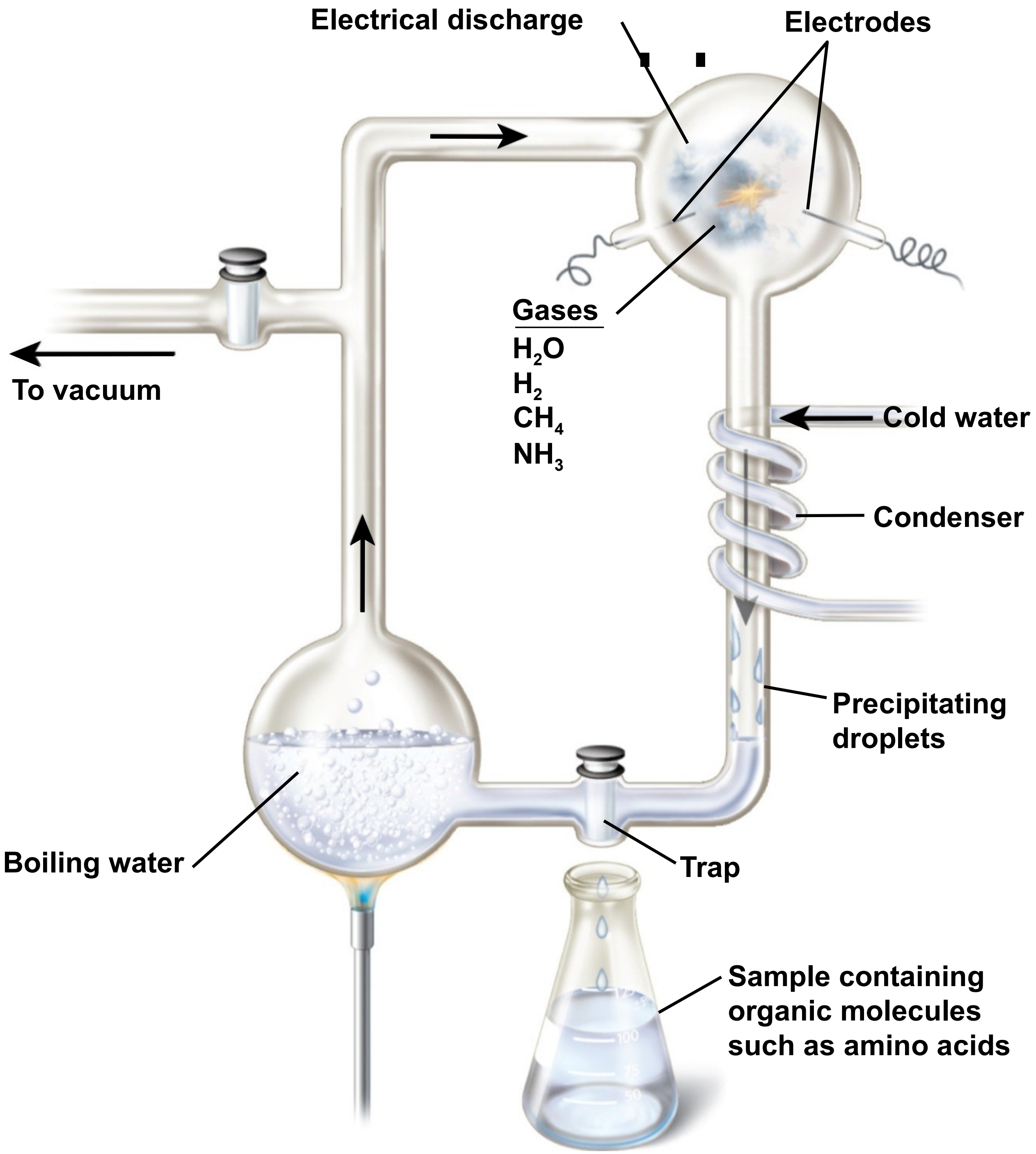
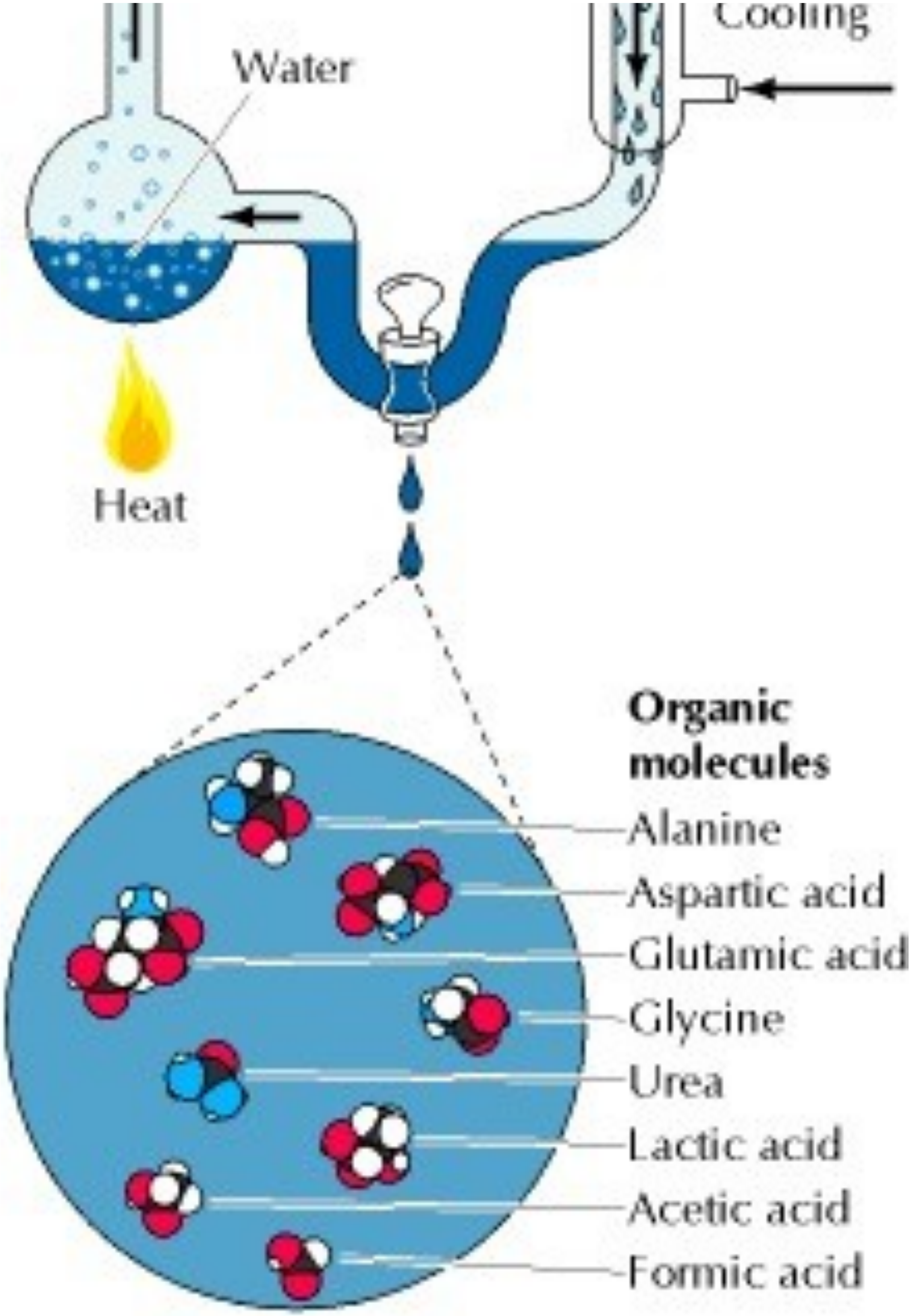



Cooling
Water
Heat
Organic molecules
Alanine
Aspartic acid
Glutamic acid
Glycine
Urea
Lactic acid
Acetic acid
Formic acid

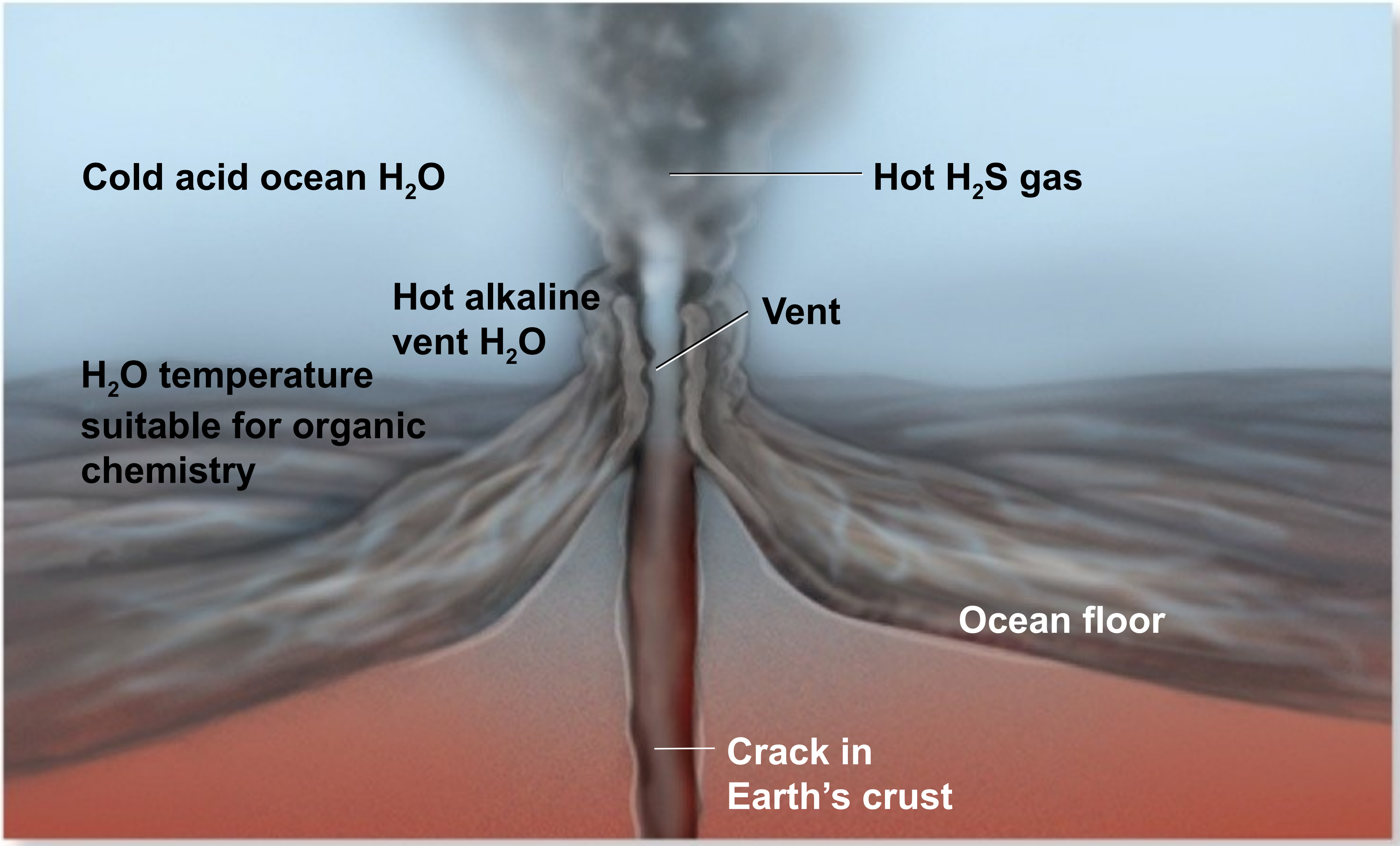
Other Hypotheses

B. Extraterrestrial hypothesis (cop out)

- ❑Meteorites brought organic carbon to Earth
  - Includes amino acids and nucleic acid bases
- ❑Opponents argue that most of this would be destroyed in the intense heating and collision

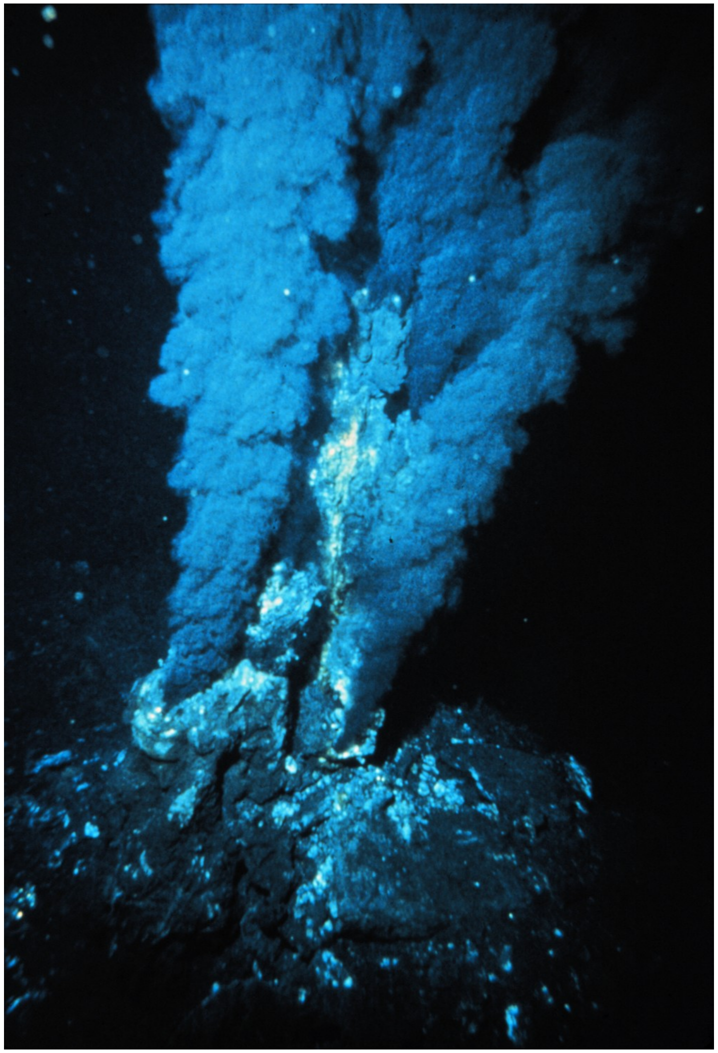
C. Deep-sea vent hypothesis

- ❑Biologically important molecules may have been formed in the temperature gradient between extremely hot vent water and cold ocean water
- ❑Complex biological communities found here that derive energy from chemicals in the vent (not the sun). Life’s origin at bottom of ocean.



(a) Deep-sea vent hypothesis "battery powered"

Deep Sea Vent “Black Smoker”



Deep sea vent community

(b) [A deep-sea vent community](#) **(6:21)**

b: © CSSF/NEPTUNE Canada

Stage 2: Organic polymers

- Experimentally, prebiotic synthesis of polymers not possible in aqueous solutions
  - ❑ Hydrolysis competes with polymerization

- Experiments have shown formation of nucleic acid polymers and polypeptides on **clay surfaces**
- Volcanic gases can cause formation of peptides from amino acids in water (prebiotic soup).

Stage 3: Formation of boundaries

- **Protobiont is**
  - An aggregate of pre-biotically produced molecules and macromolecules that has acquired a **boundary**, such as a lipid bilayer, that allows maintenance of an internal chemical environment distinct from that of its surroundings

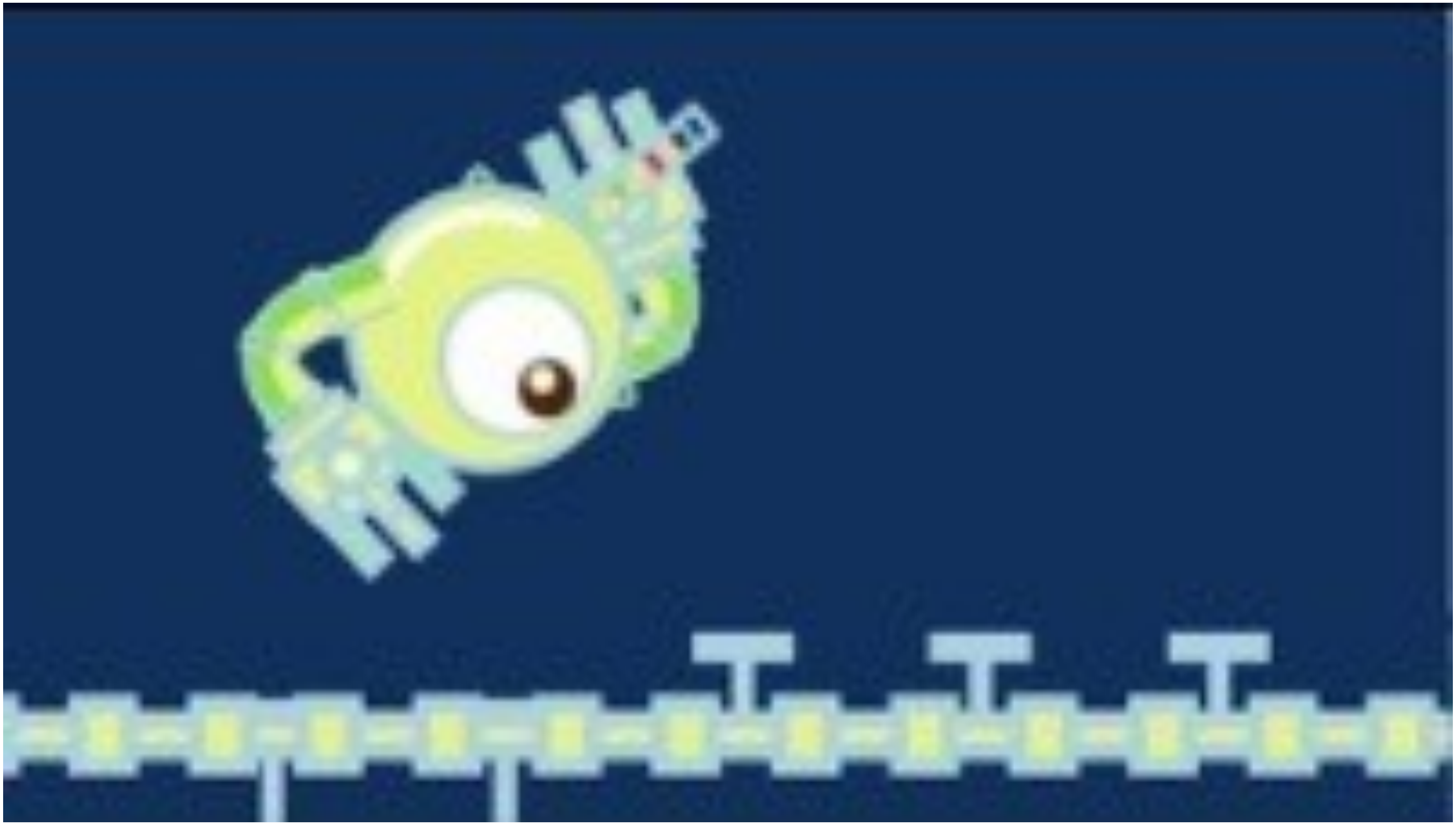
Stage 4: RNA world (3:09)

- Majority of scientists favor RNA as the first information-containing macromolecule of protobionts

- Three key RNA functions:
  1. Ability to store **information**
  2. Capacity for **self-replication**
  3. **Enzymatic function** (ribozymes)

- DNA and proteins cannot do all 3 functions

RNA World



Advantages of DNA / RNA / protein world

Information storage

- DNA would have relieved RNA of informational role and allowed RNA to do other functions
- DNA strands **more stable**, less likely to break
- DNA is less likely to suffer mutations (**correcting mechanisms**)

Metabolism and other cellular functions

- Proteins have a greater catalytic potential and efficiency
- Proteins can perform other tasks – cytoskeleton, transport, etc.

Eon	Era	Period	Date	Events
Hadean			4.6-3.8bya	Formation of earth
Archeon			3.8-2.5bya	1st fossils: prokaryotes
				1st cyanobacteria
				stromatolites
Proterozoic			2.5bya-540mya	1st continents
				Toxic buildup of oxygen
				1st eukaryotes
				1st multicellular organisms
Phanerozoic			540mya-present	
	Paleozoic		540-250mya	**Age of fishes**
				Cambrian explosion
				1st vertebrates
				1st arthropods
				1st seed plants
				1st reptiles/amniotic eggs
				Pangaea
				Largest recorded extinction
	Mesozoic		250-65mya	**Age of reptiles**
		Triassic		1st mammals
				Little dinosaurs
		Jurassic		1st birds
				Dinosaurs ruled!
		Cretaceous		1st flowering plants
				Mass extinction
				End of dinosaurs
	Cenozoic		65mya	**Age of mammals**
		Tertiary		Marine mammals
			7mya	1st Hominoids
		Quaternary	1.8mya-present	Neanderthals
			200,000ya	Modern humans

Cosmos Magazine: The big 5 mass extinctions

https://cosmosmagazine.com/palaeontology/big-five-extinctions

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Trilobites were the most diverse and abundant of the animals that appeared in the Cambrian explosion 550 million years ago. Their great success was helped by their spiky armor and multifaceted eyes. They survived the first great extinction but were nearly wiped out in the second. The likely culprit was the newly evolved land plants that emerged, covering the planet during the Devonian period. Their deep roots stirred up the earth, releasing nutrients into the ocean. This might have triggered algal blooms which sucked oxygen out of the water, suffocating bottom dwellers like the trilobites.

End Permian, 251 million years ago, 96% of species lost — Tabulate coral, 5 CM

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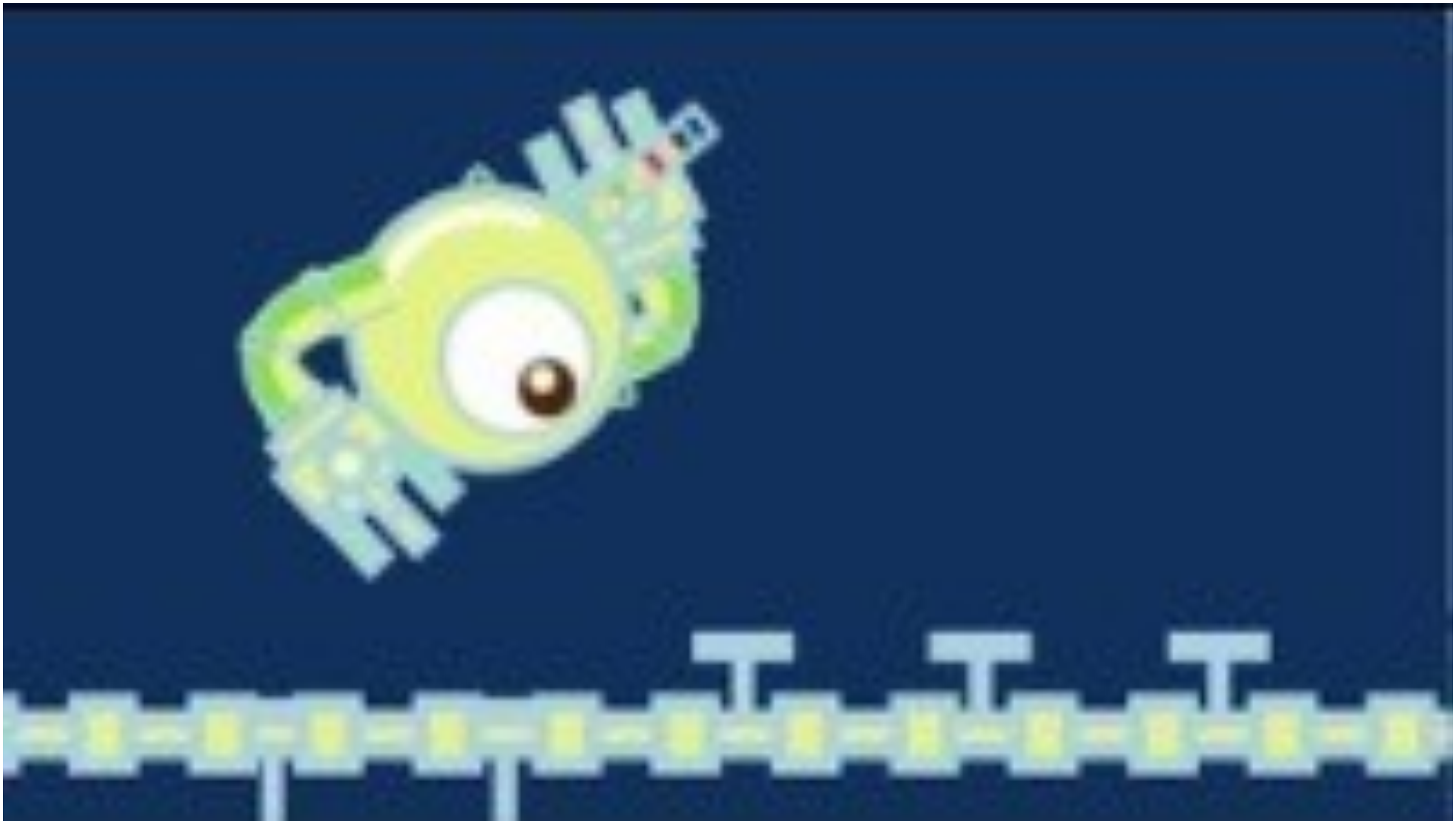

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2. The Fossil Record

- Preserved remains of past life on Earth
- Many (most) rocks with fossils are sedimentary
  - ❑Sediments pile up and become rock
  - ❑Organisms buried quickly, hard parts replaced by minerals
- Older rock is deeper and older organisms are deeper in the rock bed

Radioisotope dating (4:17)

- Fossils can be dated using elemental isotopes (radioisotopes=unstable) in accompanying rock. (isotopes differ in # of neutrons)
- **Half-life** – length of time required for exactly one-half of original isotope to decay into another isotope
- Measure amount of a given isotope as well as the amount of the decay product
- Expect fossil record to underestimate actual date species came into existence

Dating Fossils

4:05 min

How does radiocarbon dating work?

2 min

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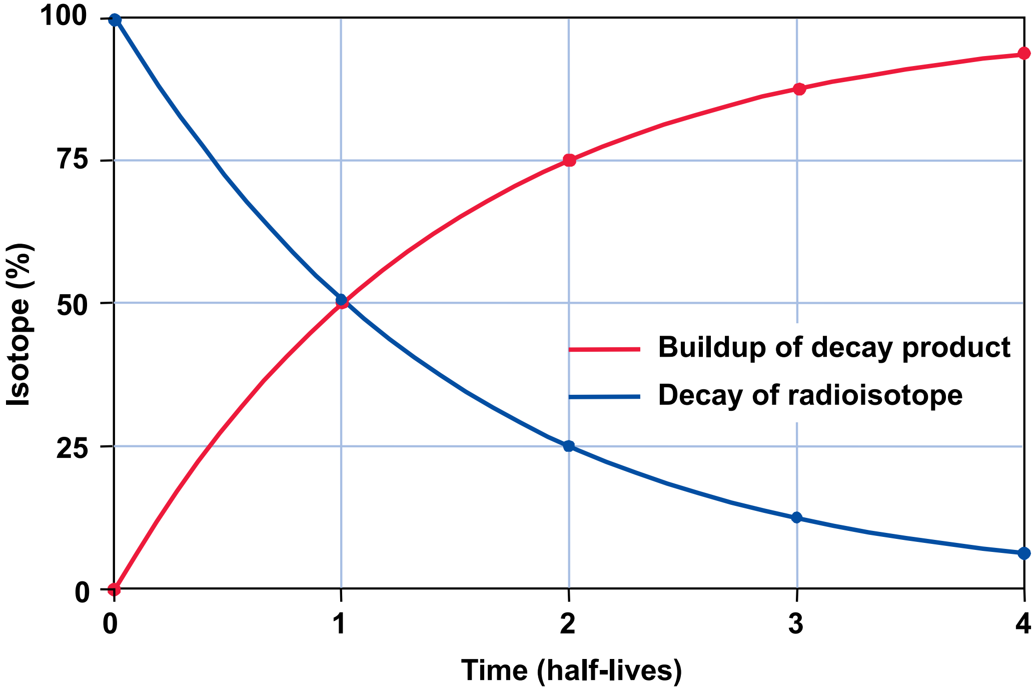

(a) Decay of a radioisotope

Radioisotope	Decay product	Half-life (years)	Useful dating range (years)
Carbon-14	Nitrogen-14	5,730	100–50,000
Potassium-40	Argon-40	1.3 billion	100,000–4.5 billion
Rubidium-87	Strontium-87	47 billion	10million–4.5 billion
Uranium-235	Lead-207	710 million	10million–4.5 billion
Uranium-238	Lead-206	4.5 billion	10million–4.5 billion

(b) How does radiocarbon dating work? (2:11)

How Carbon Dating Works

3:30 min

3. History of Life on Earth

- Geological time scale
  - Origin 4.55 bya to present

- Four eons
  - **Hadean**
  - **Archean**
  - **Proterozoic**
  - **Phanerozoic** (starts with Cambrian period) 570 mya

Precambrian (before Cambrian period)

- Each eon further divided into eras

Prokaryotic cells arose during Archaeon Eon (4-2.5bya)

- Archean Eon – when diverse microbial life flourished in primordial oceans
- **First known fossils 3.5 bya**
- First cells prokaryotic
- All life forms prokaryotic during Archaeon Eon
- Hardly any free oxygen so organisms were **anaerobic**
- Autotrophs evolved (called cyanobacteria) as the supply of organic molecules dwindled (3.5-3 bya)

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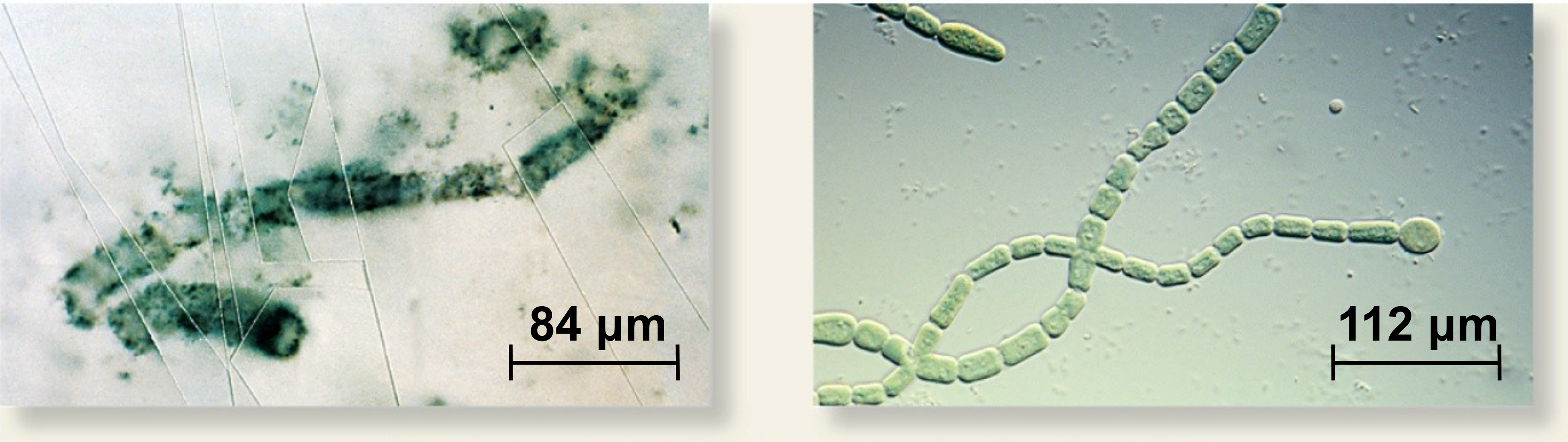
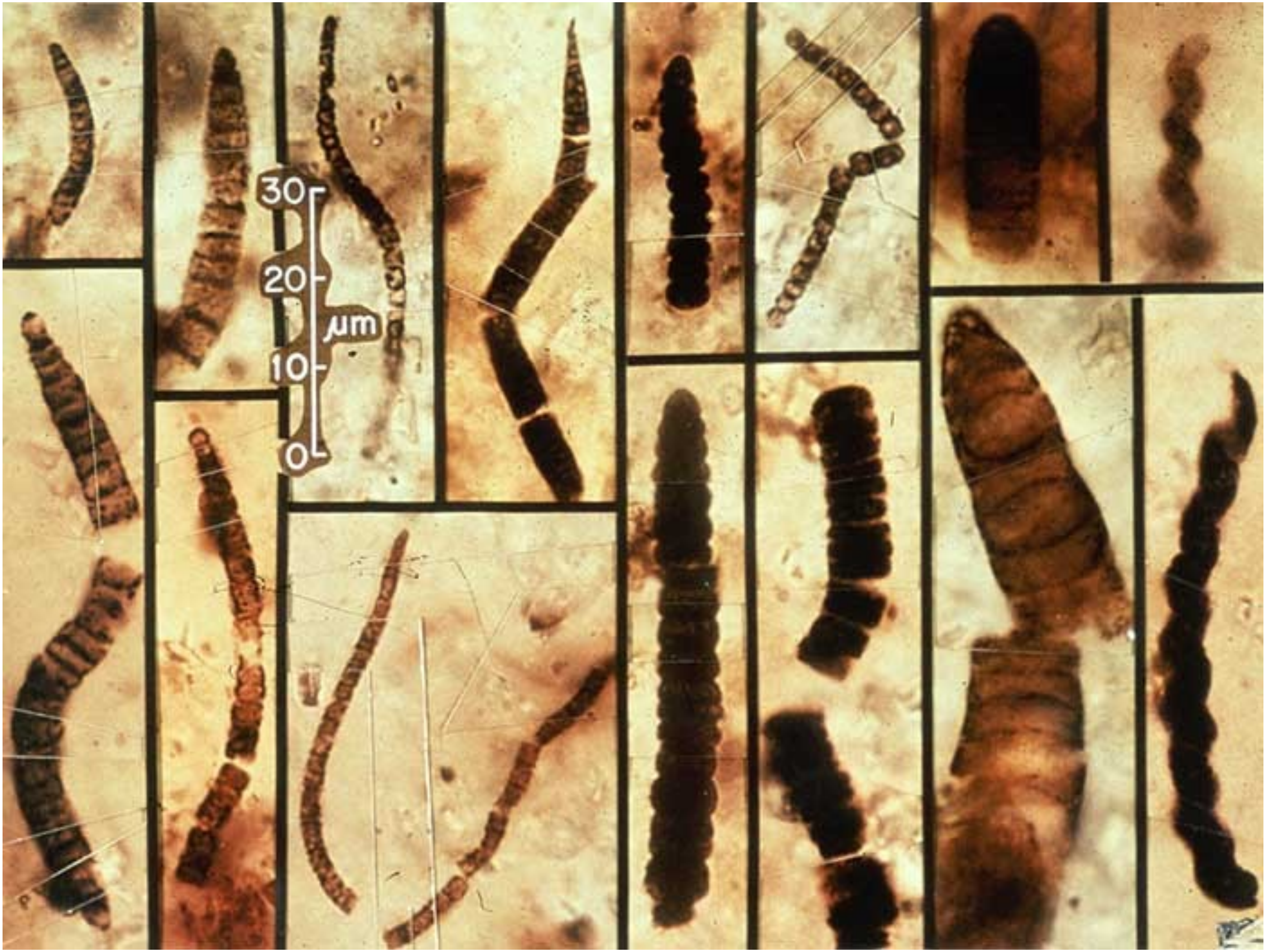


(a) Fossil prokaryote **(b) Modern cyanobacteria**

a: © Stanley M. Awramik/Biological Photo Service; b: © Michael Abbey/Visuals Unlimited

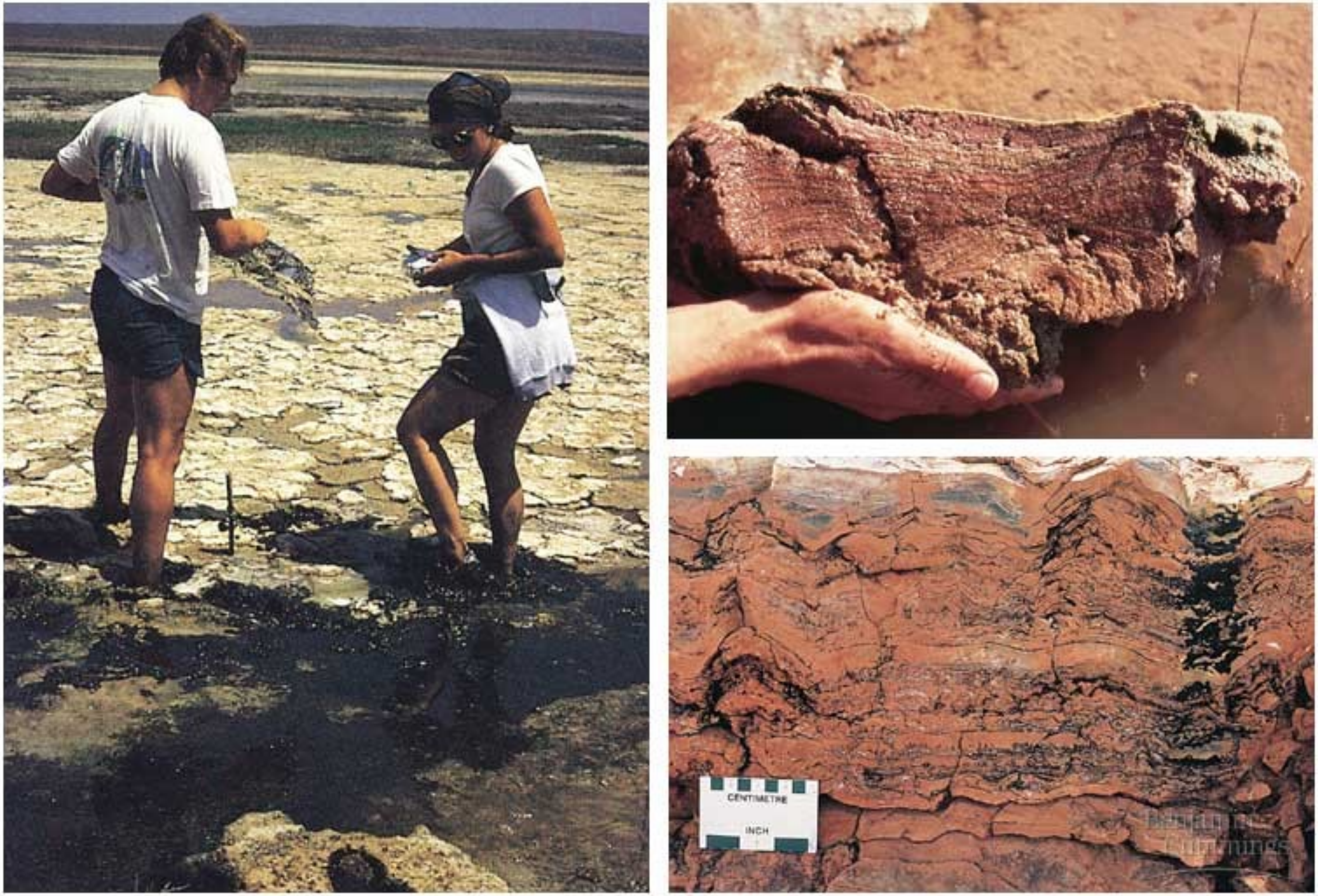
Filamentous cyanobacteria from the Bitter Springs Chert in central Australia



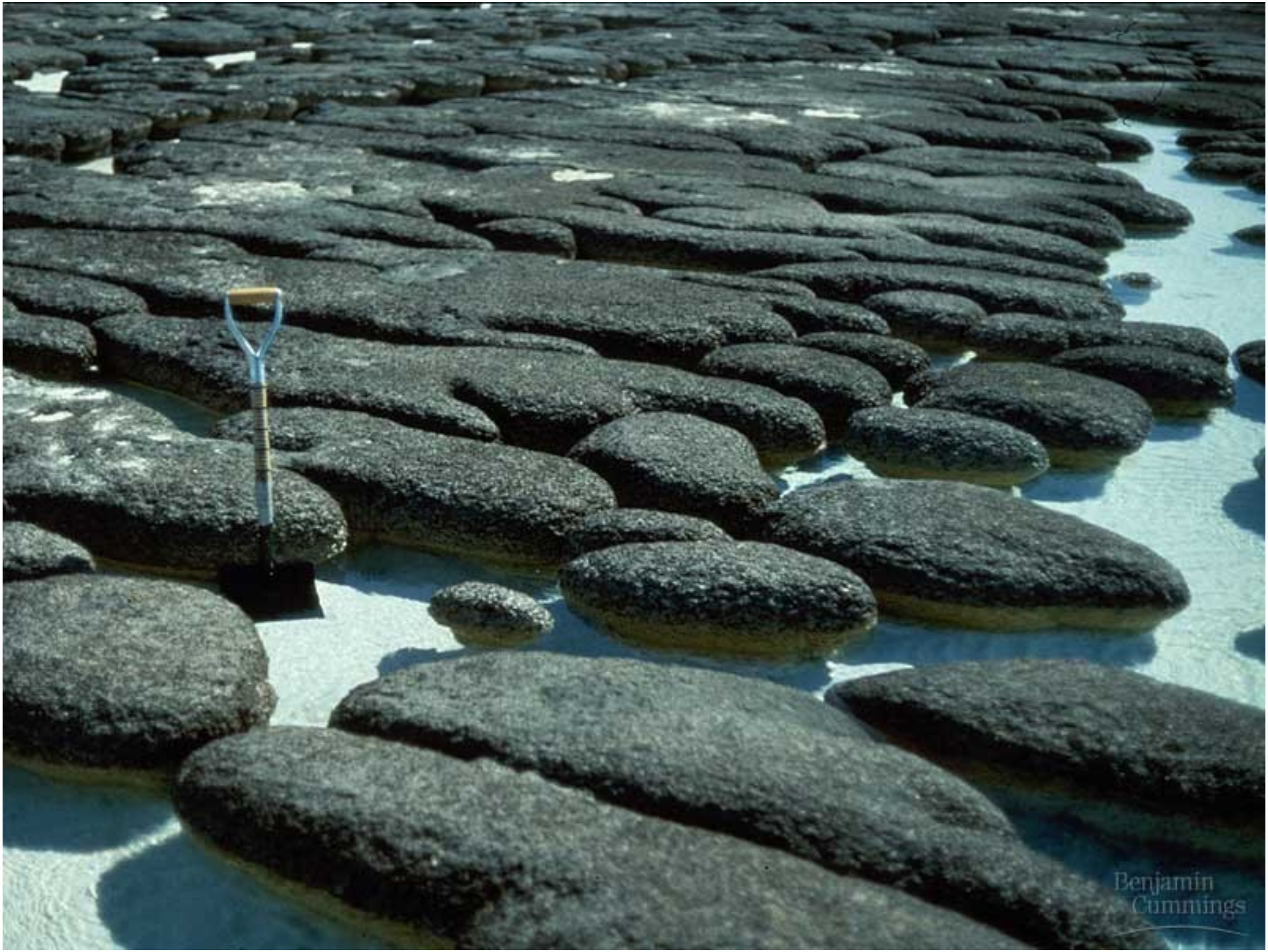
Stromatolites

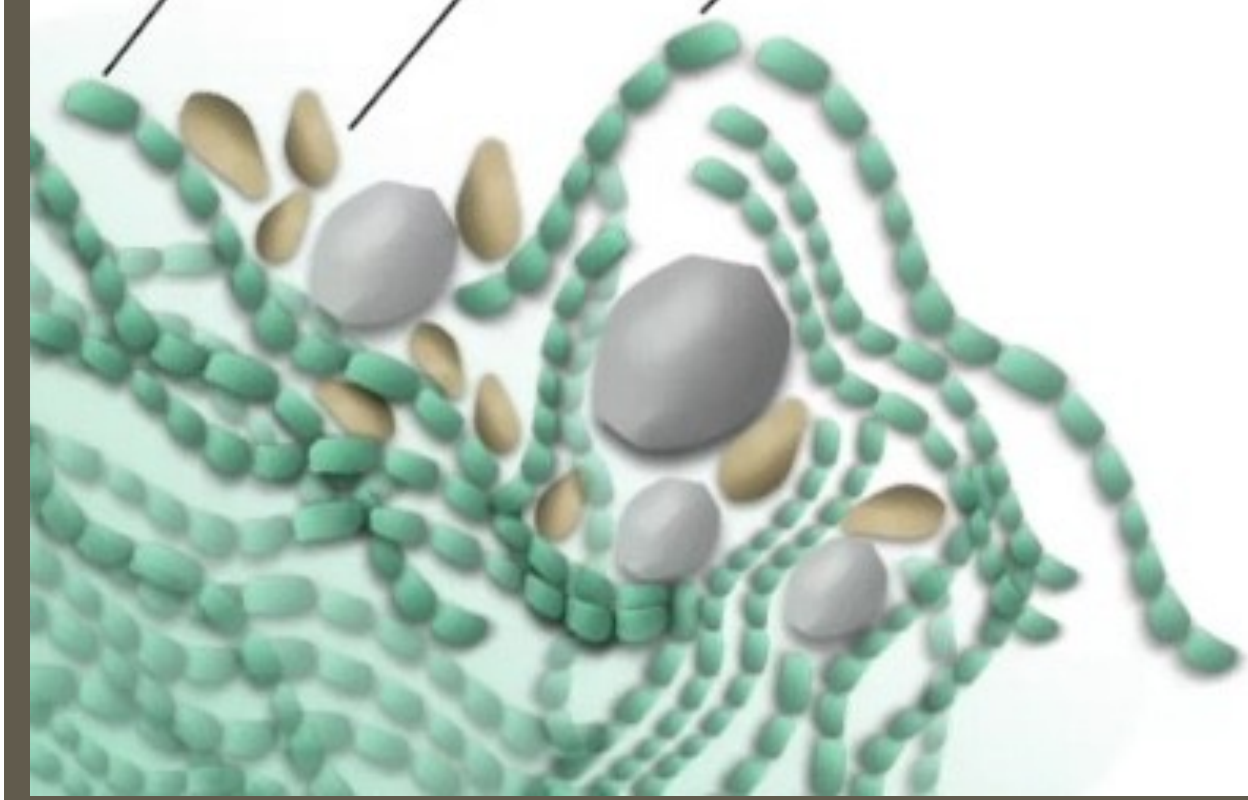
- Autotrophic cyanobacteria were preserved when heterotrophic ancestors were not
- Form **stromatolites** – large mats with layered structure of calcium carbonate (3.7bya earliest)
- Cyanobacteria produce **oxygen** as a waste product of photosynthesis
- Spelled doom for many prokaryotic groups that were anaerobic
- Allowed the evolution of aerobic species

Bacterial mats and stromatolites

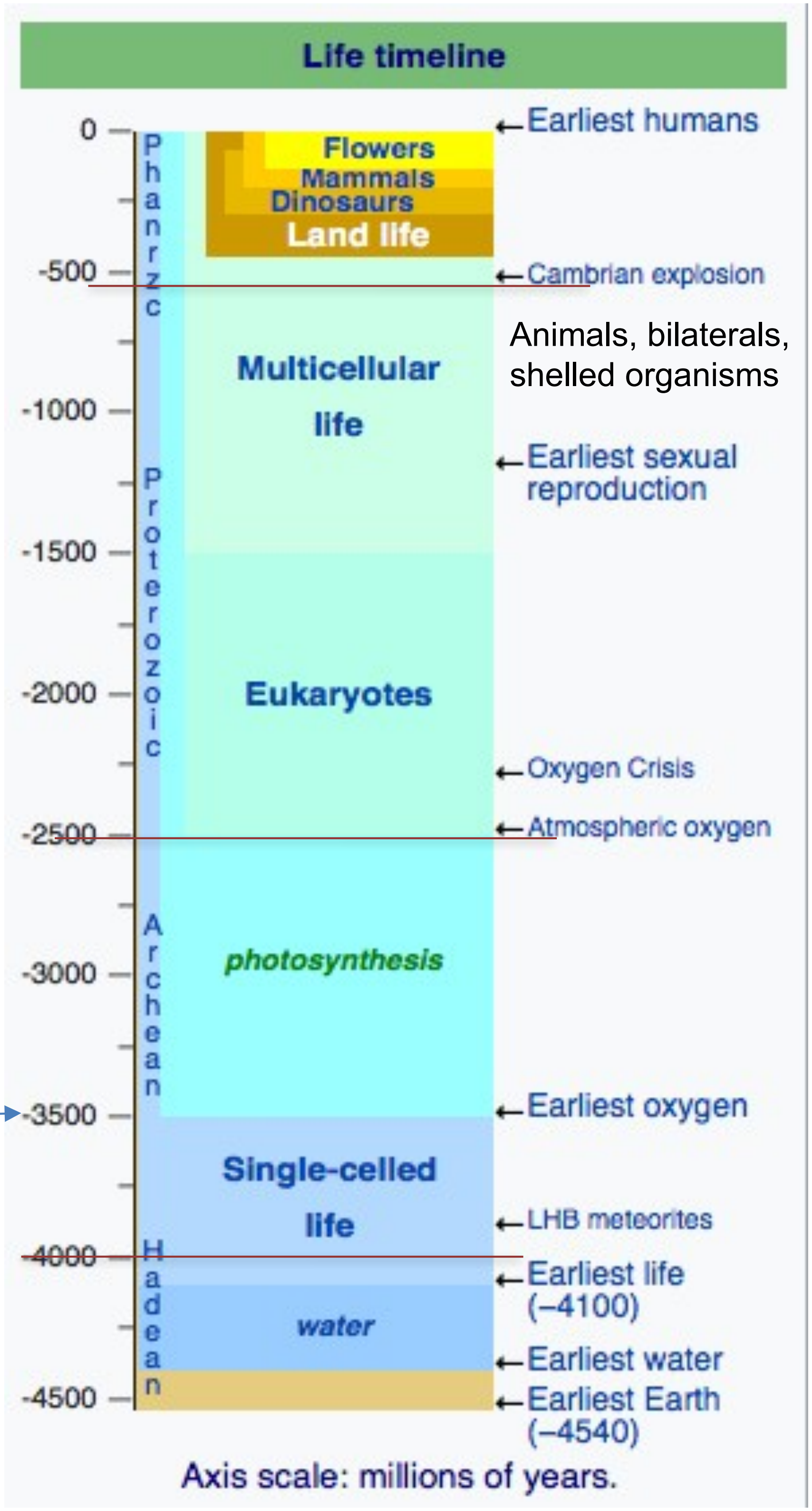


Stromatolites in Northern Canada





1. Microorganisms live on the surface of the stromatolite
2. Sediment is deposited on the microorganisms
3. The microorganisms react by growing upward through the sediment, forming a new layer



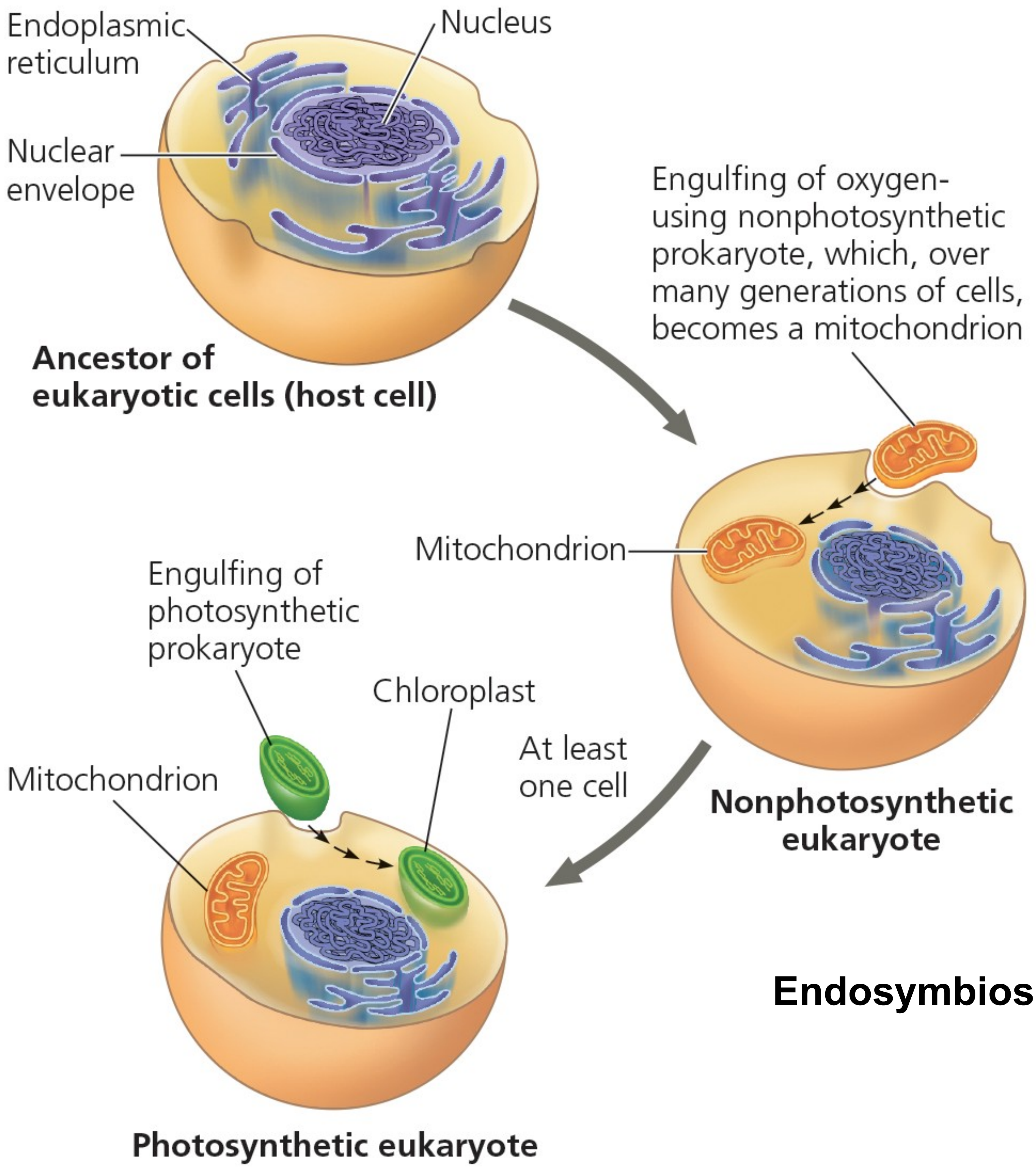
Animals, bilaterals, shelled organisms

Stromatolites appear

The Origin of Eukaryotic Cells Involved a Union Between Bacterial and Archaeal Cells

- In modern eukaryotes, DNA is found in nucleus, mitochondria and chloroplasts
- Examine properties of this DNA and compare to modern prokaryotes
- Nuclear genome – both Bacteria (metabolism, respiration) and Archaea (replication, expression) contributed substantially

☐ **Endosymbiotic** (OS 20.3)– one organism lives inside another
  - Data supports this origin


Endoplasmic reticulum
Nucleus
Nuclear envelope
Ancestor of eukaryotic cells (host cell)
Engulfing of oxygen-using nonphotosynthetic prokaryote, which, over many generations of cells, becomes a mitochondrion
Mitochondrion
Nonphotosynthetic eukaryote
At least one cell
Engulfing of photosynthetic prokaryote
Chloroplast
Mitochondrion
Photosynthetic eukaryote

Endosymbiosis

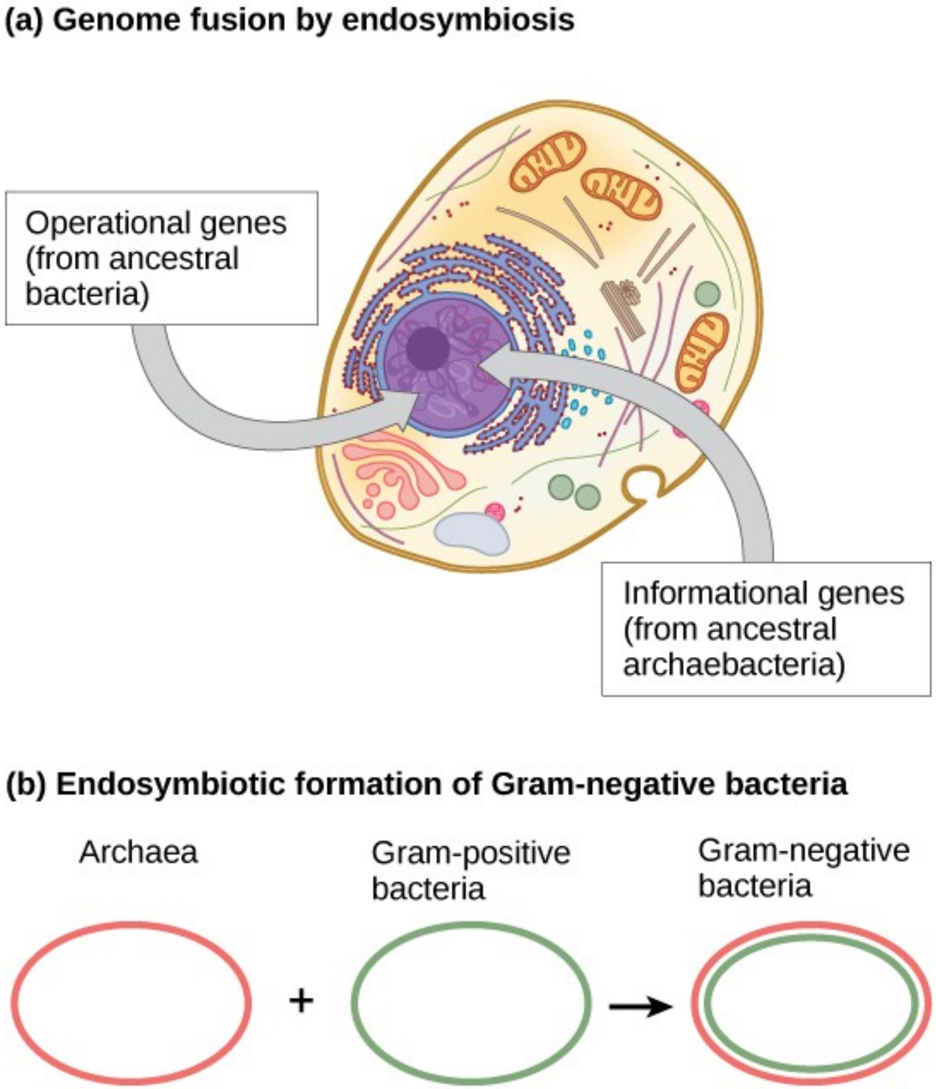
1.Mitochondria and chloroplasts have double membranes.

2. Both have ribosomes and circular DNA molecules like prokaryotes.

3. Both are mostly independent organelles that grow and reproduce within the cell.

Figure 20.14

- The theory that mitochondria and chloroplasts are endosymbiotic in origin is now widely accepted. More controversial is the proposal that (a) the eukaryotic nucleus resulted from the fusion of archaeal and bacterial genomes, and that (b) Gram-negative bacteria, which have two membranes, resulted from the fusion of Archaea and Gram-positive bacteria, each of which has a single membrane.


(a) Genome fusion by endosymbiosis
Operational genes (from ancestral bacteria)
Informational genes (from ancestral archaebacteria)
(b) Endosymbiotic formation of Gram-negative bacteria
Archaea
+
Gram-positive bacteria
Gram-negative bacteria

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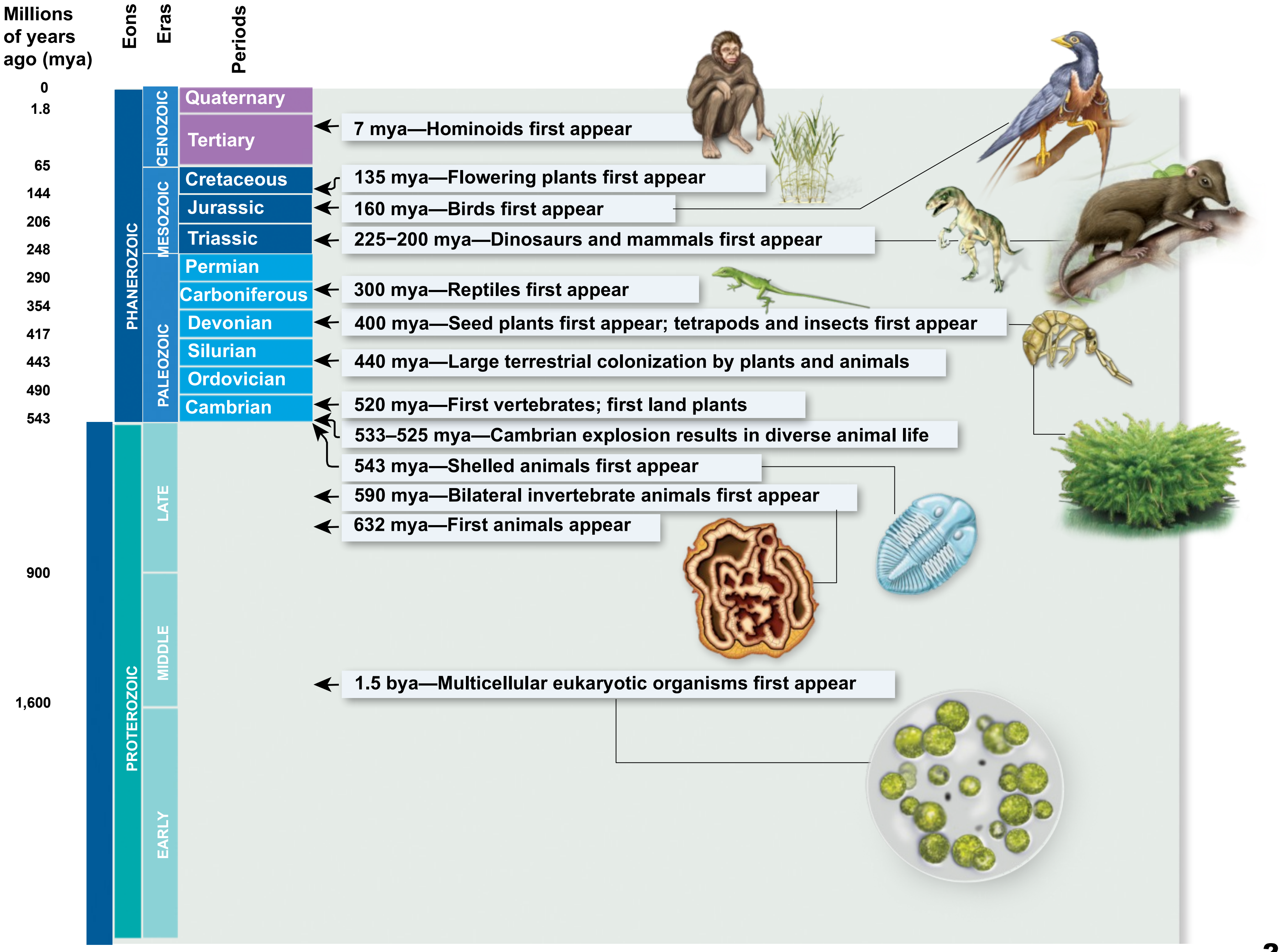


Millions of years ago (mya)	Eons	Eras	Periods
0	PHANEROZOIC	CENOZOIC	Quaternary
1.8			Tertiary
65		MESOZOIC	Cretaceous
144			Jurassic
206			Triassic
248		PALEOZOIC	Permian
290			Carboniferous
354			Devonian
417			Silurian
443			Ordovician
490			Cambrian
543	PROTEROZOIC	LATE	
900		MIDDLE	
1,600		EARLY	

7 mya—Hominoids first appear

135 mya—Flowering plants first appear

160 mya—Birds first appear

225–200 mya—Dinosaurs and mammals first appear

300 mya—Reptiles first appear

400 mya—Seed plants first appear; tetrapods and insects first appear

440 mya—Large terrestrial colonization by plants and animals

520 mya—First vertebrates; first land plants

533–525 mya—Cambrian explosion results in diverse animal life

543 mya—Shelled animals first appear

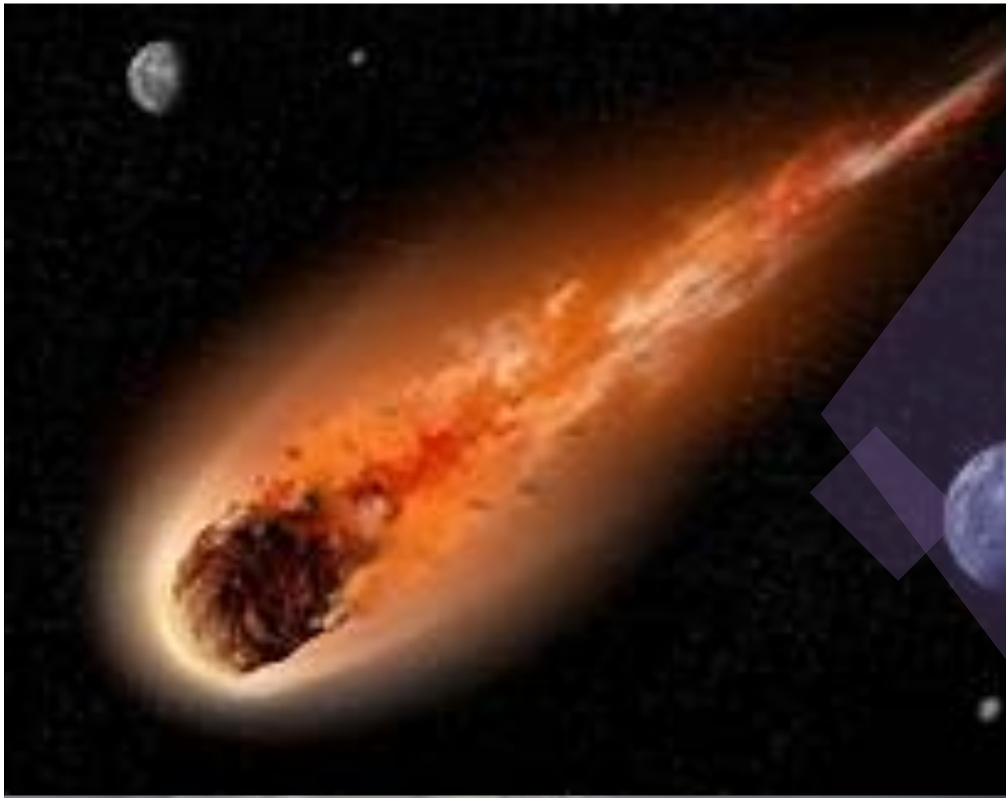
590 mya—Bilateral invertebrate animals first appear

632 mya—First animals appear

1.5 bya—Multicellular eukaryotic organisms first appear

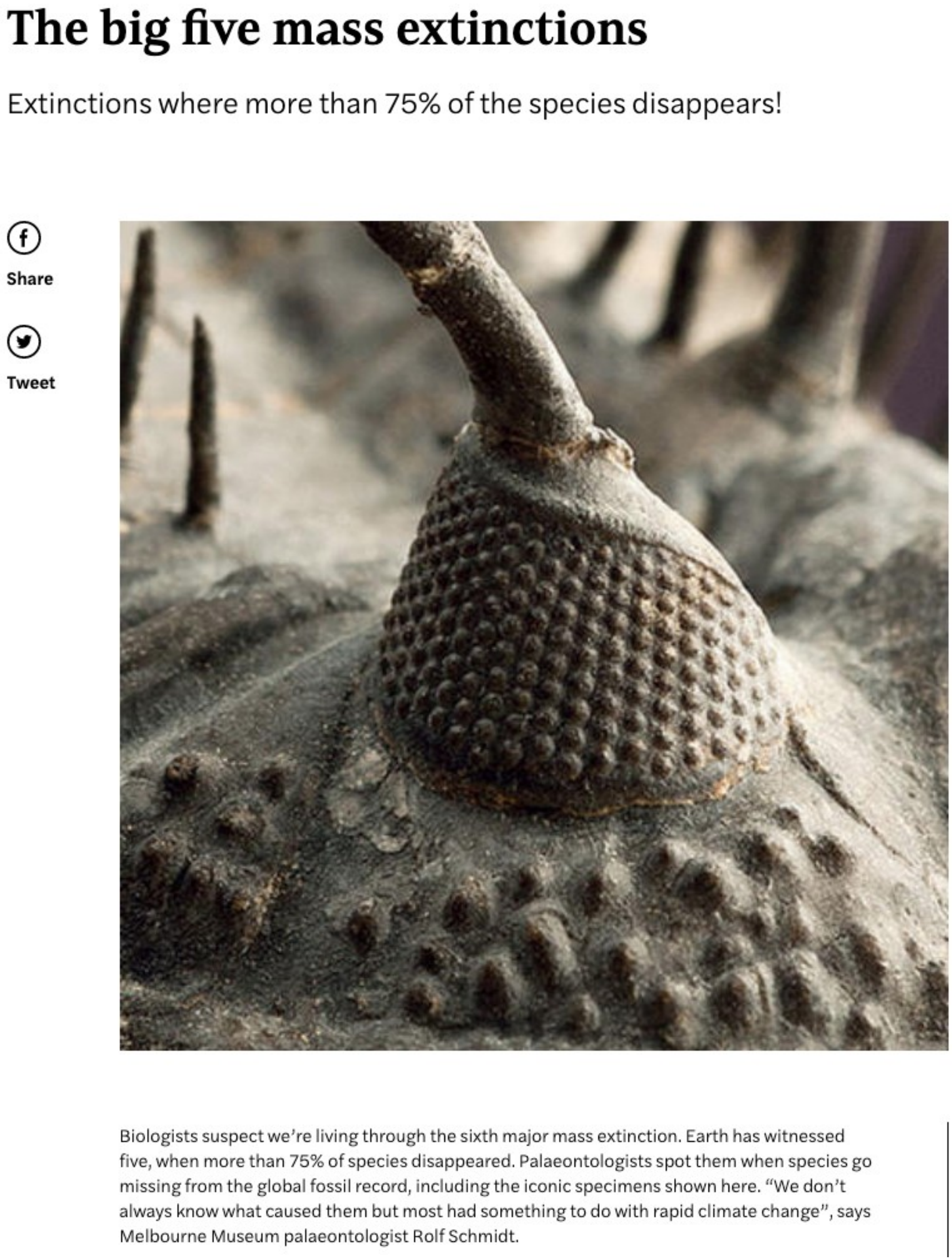
Major environmental changes (**SELECTION PRESSURES**)

- Climate/temperature/water (over the last 2 billion yrs = major flux)
- Atmosphere (changed over 4 billion yrs)
- Land masses formed (during Archaean) = Aquatic/terrestrial. Then continental drift.
- Floods + Glaciation. Snowball Earth hypothesis: all covered in ice 790-630 mya.
- Volcanic eruptions
- Meteoric impacts = mass extinctions



Mass extinctions have occurred

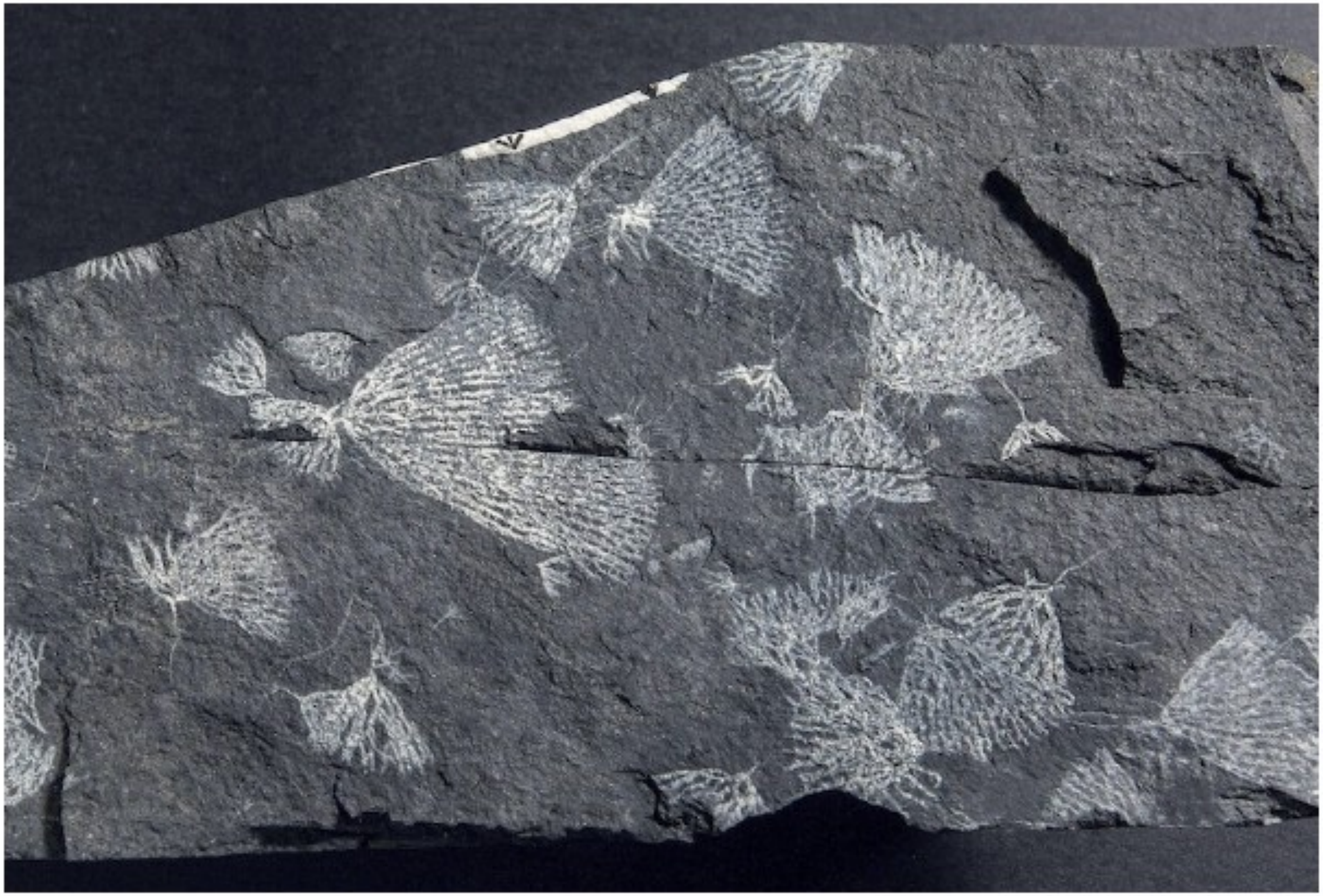
- 5 large mass extinctions
- Near end of **Ordovician, Devonian, Permian, Triassic**, and **Cretaceous** periods
- Boundaries between geologic time periods are often based on these events
- Rapid extinction of many modern species due to human activities is sometimes referred to as the **sixth mass extinction**



The big five mass extinctions

Extinctions where more than 75% of the species disappears!

Biologists suspect we're living through the sixth major mass extinction. Earth has witnessed five, when more than 75% of species disappeared. Palaeontologists spot them when species go missing from the global fossil record, including the iconic specimens shown here. "We don't always know what caused them but most had something to do with rapid climate change", says Melbourne Museum palaeontologist Rolf Schmidt.



Credit: Jaime Murcia/Museum Victoria

End Ordovician, 444 million years ago, 86% of species lost – Graptolite 2-3 cm length

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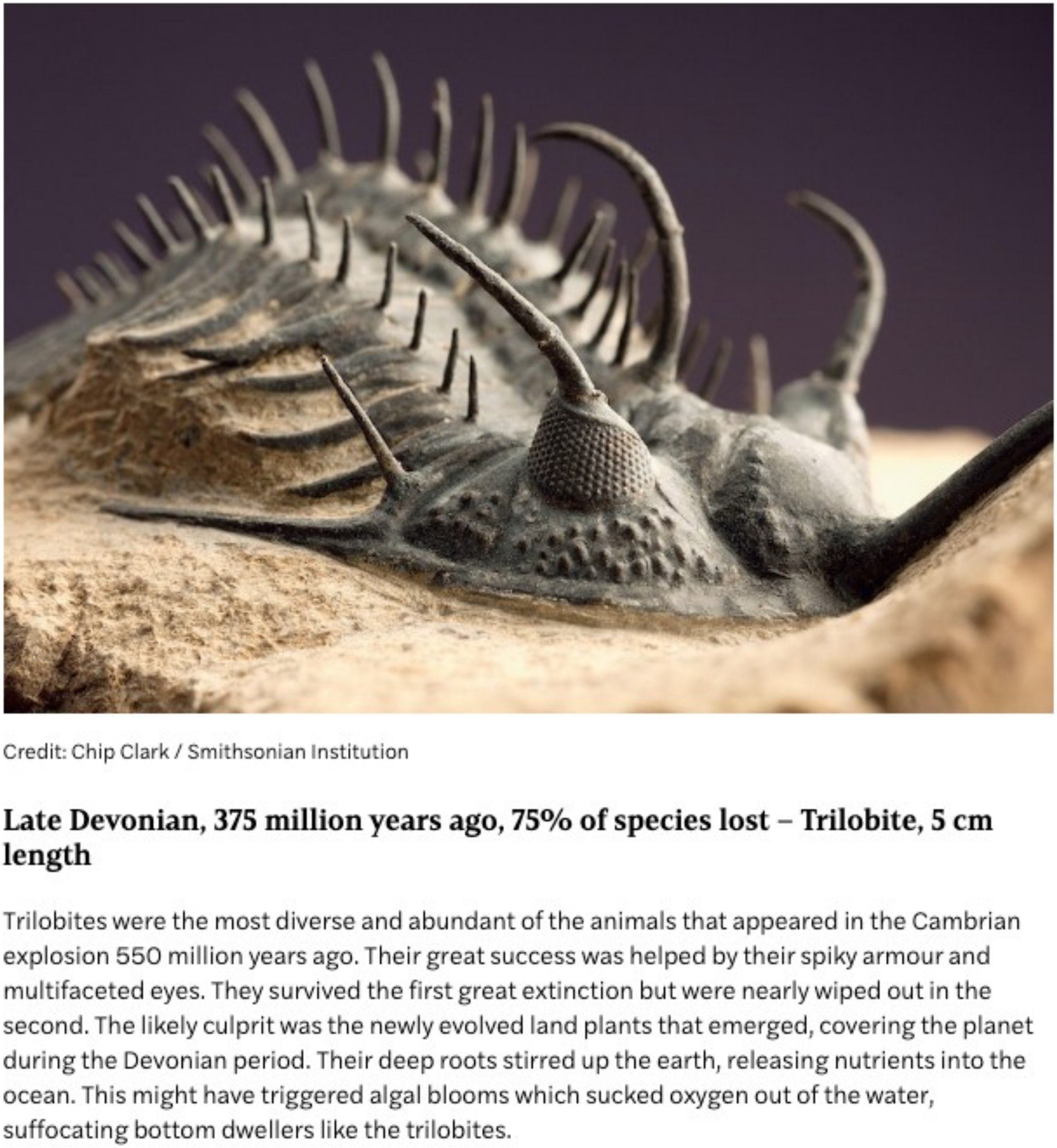

Credit: Chip Clark / Smithsonian Institution

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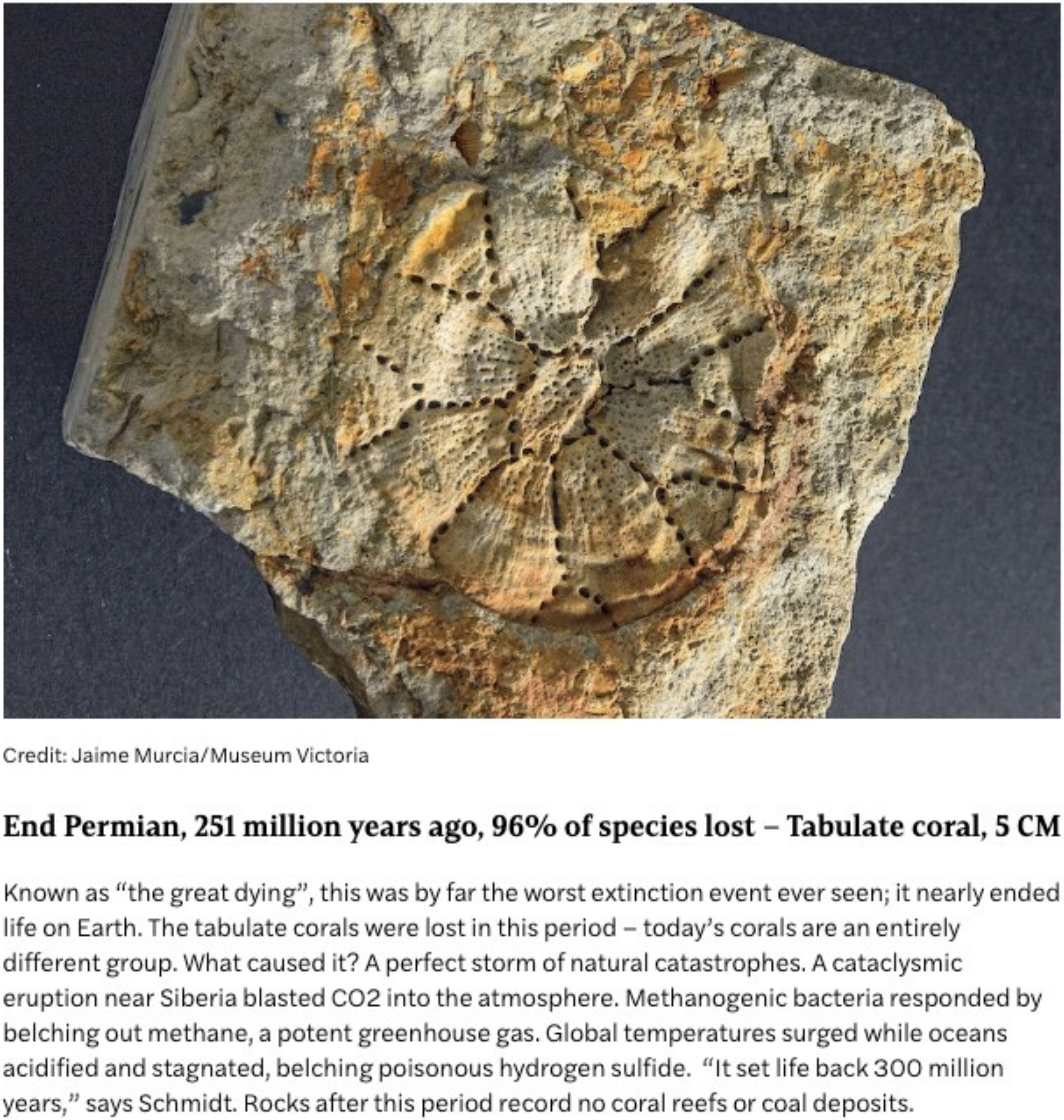

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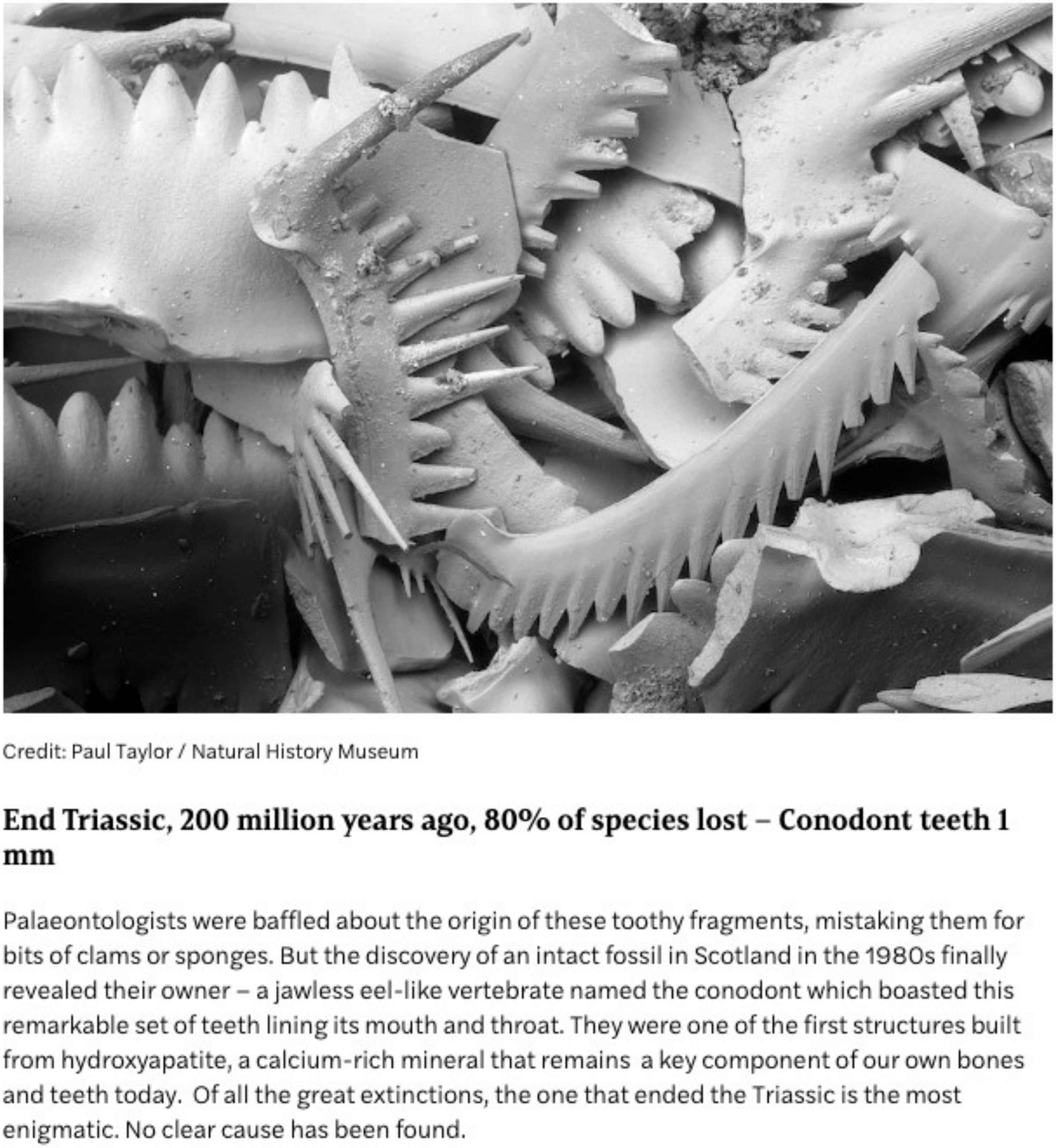
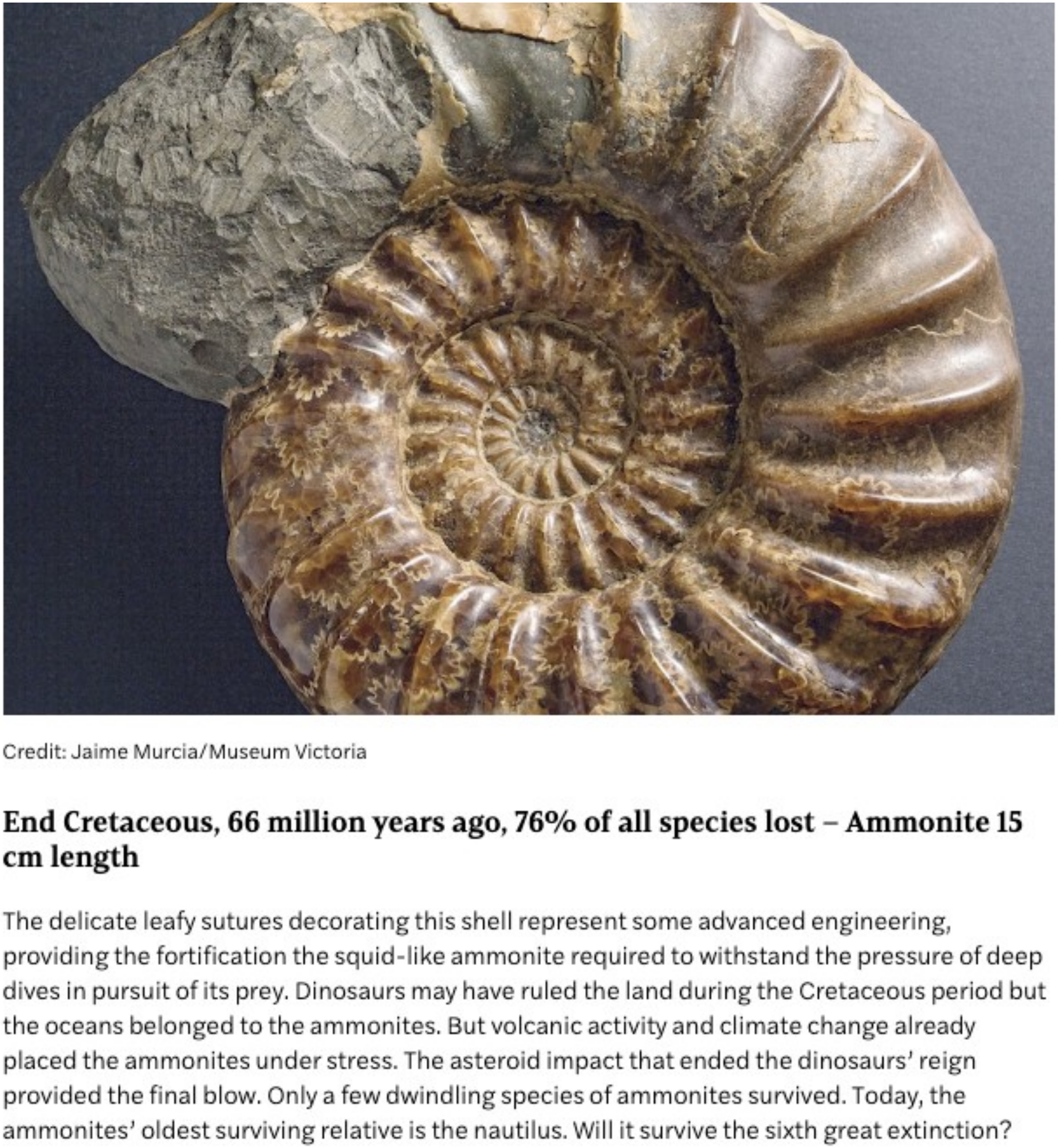
Known as “the great dying”, this was by far the worst extinction event ever seen; it nearly ended life on Earth. The tabulate corals were lost in this period – today’s corals are an entirely different group. What caused it? A perfect storm of natural catastrophes. A cataclysmic eruption near Siberia blasted CO2 into the atmosphere. Methanogenic bacteria responded by belching out methane, a potent greenhouse gas. Global temperatures surged while oceans acidified and stagnated, belching poisonous hydrogen sulfide. “It set life back 300 million years,” says Schmidt. Rocks after this period record no coral reefs or coal deposits.



Credit: Paul Taylor / Natural History Museum

End Triassic, 200 million years ago, 80% of species lost – Conodont teeth 1 mm

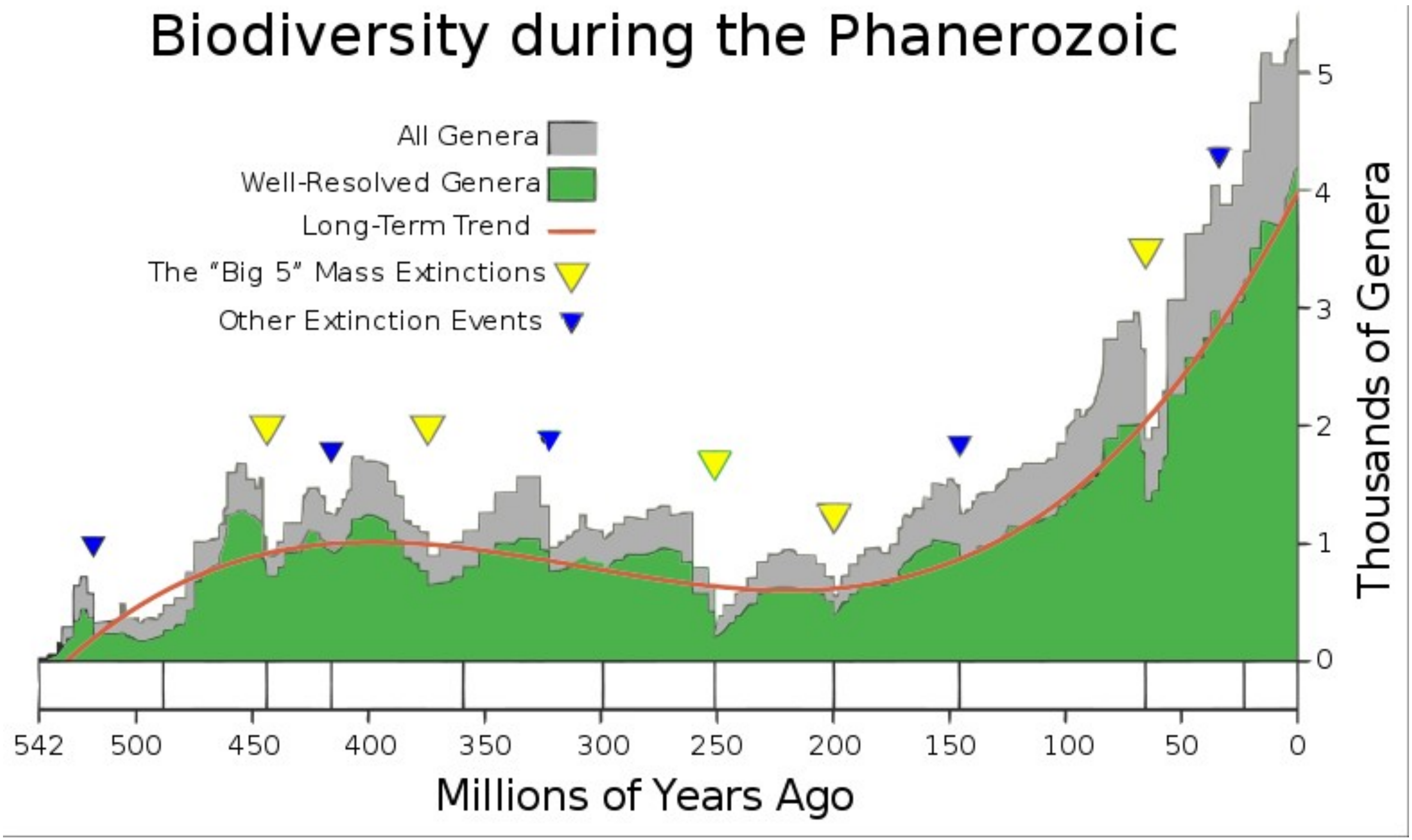
Palaeontologists were baffled about the origin of these toothy fragments, mistaking them for bits of clams or sponges. But the discovery of an intact fossil in Scotland in the 1980s finally revealed their owner – a jawless eel-like vertebrate named the conodont which boasted this remarkable set of teeth lining its mouth and throat. They were one of the first structures built from hydroxyapatite, a calcium-rich mineral that remains a key component of our own bones and teeth today. Of all the great extinctions, the one that ended the Triassic is the most enigmatic. No clear cause has been found.



Credit: Jaime Murcia/Museum Victoria

End Cretaceous, 66 million years ago, 76% of all species lost – Ammonite 15 cm length

The delicate leafy sutures decorating this shell represent some advanced engineering, providing the fortification the squid-like ammonite required to withstand the pressure of deep dives in pursuit of its prey. Dinosaurs may have ruled the land during the Cretaceous period but the oceans belonged to the ammonites. But volcanic activity and climate change already placed the ammonites under stress. The asteroid impact that ended the dinosaurs' reign provided the final blow. Only a few dwindling species of ammonites survived. Today, the ammonites' oldest surviving relative is the nautilus. Will it survive the sixth great extinction?


Biodiversity during the Phanerozoic
All Genera
Well-Resolved Genera
Long-Term Trend
The "Big 5" Mass Extinctions
Other Extinction Events
Thousands of Genera
0
1
2
3
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5
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450
400
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150
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50
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Millions of Years Ago

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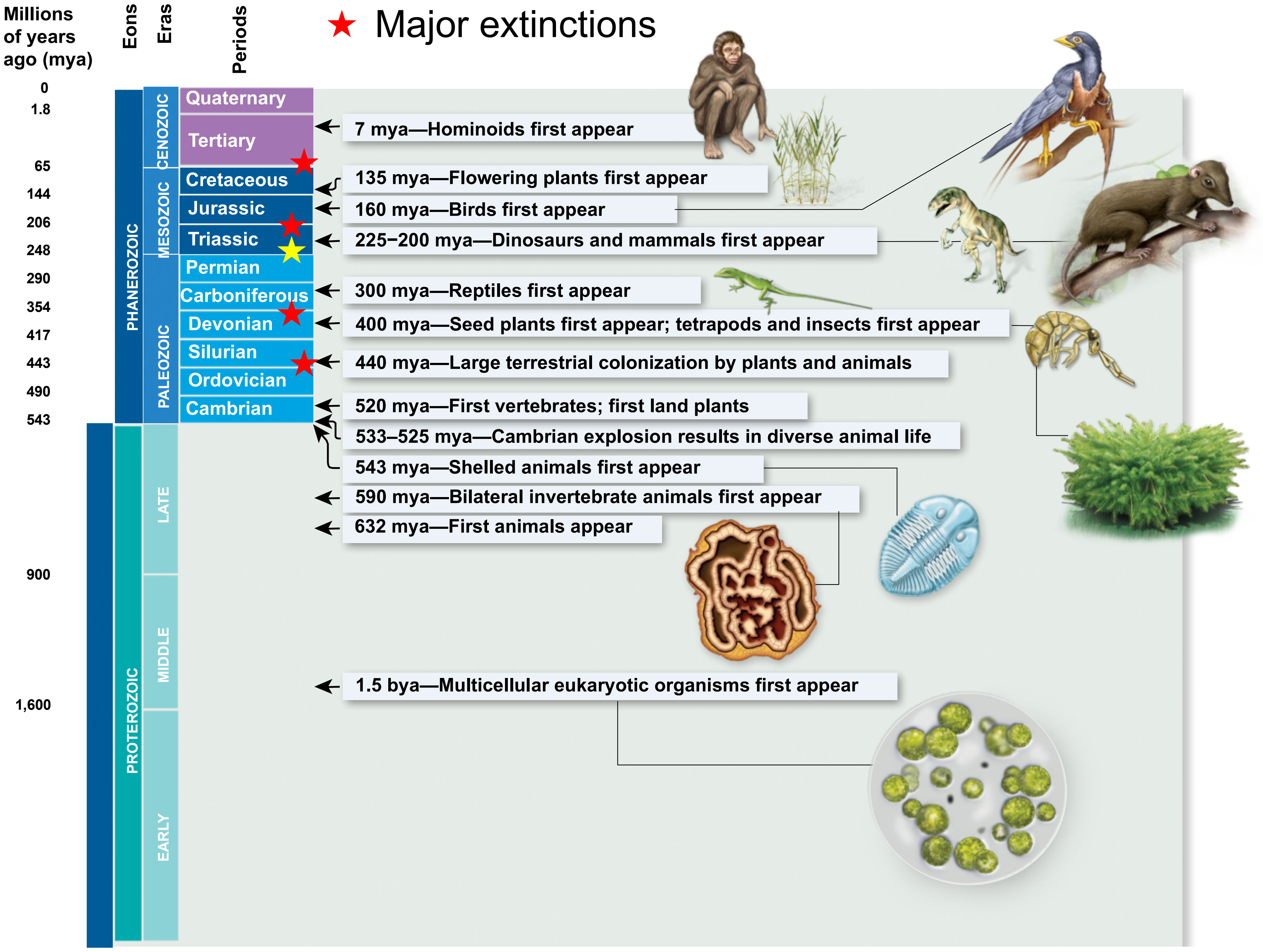
★ Major extinctions



Millions of years ago (mya)	Eons	Eras	Periods
0	PHANEROZOIC	CENOZOIC	Quaternary
1.8			Tertiary ★
65		MESOZOIC	Cretaceous
144			Jurassic ★
206			Triassic ★
248		PALEOZOIC	Permian
290			Carboniferous
354			Devonian ★
417			Silurian ★
443			Ordovician
490			Cambrian
543	PROTEROZOIC	LATE	
900		MIDDLE	
1,600		EARLY	

7 mya—Hominoids first appear

135 mya—Flowering plants first appear

160 mya—Birds first appear

225–200 mya—Dinosaurs and mammals first appear

300 mya—Reptiles first appear

400 mya—Seed plants first appear; tetrapods and insects first appear

440 mya—Large terrestrial colonization by plants and animals

520 mya—First vertebrates; first land plants

533–525 mya—Cambrian explosion results in diverse animal life

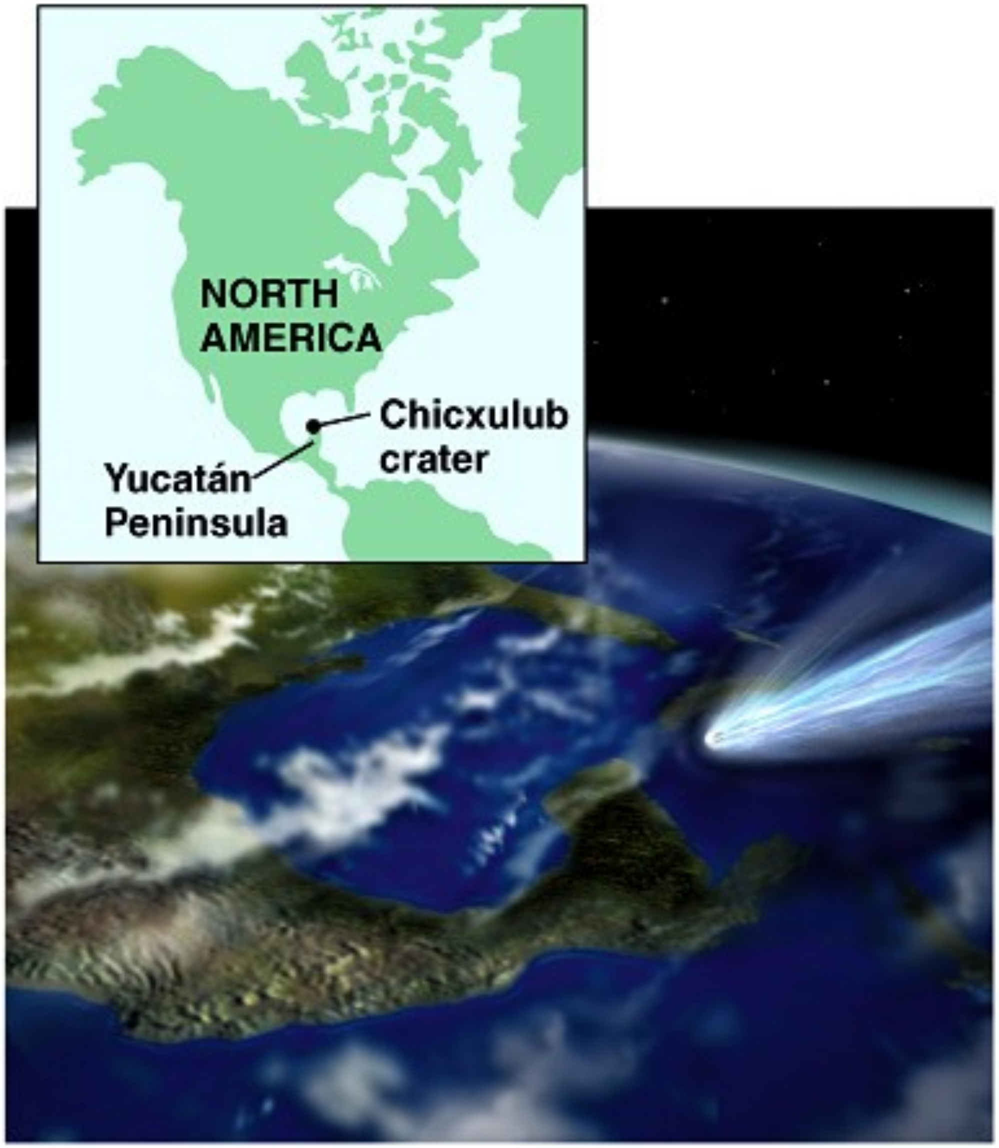
543 mya—Shelled animals first appear

590 mya—Bilateral invertebrate animals first appear

632 mya—First animals appear

1.5 bya—Multicellular eukaryotic organisms first appear

Trauma for Earth (asteroid) and its Cretaceous life (66mya) End of dinosaurs



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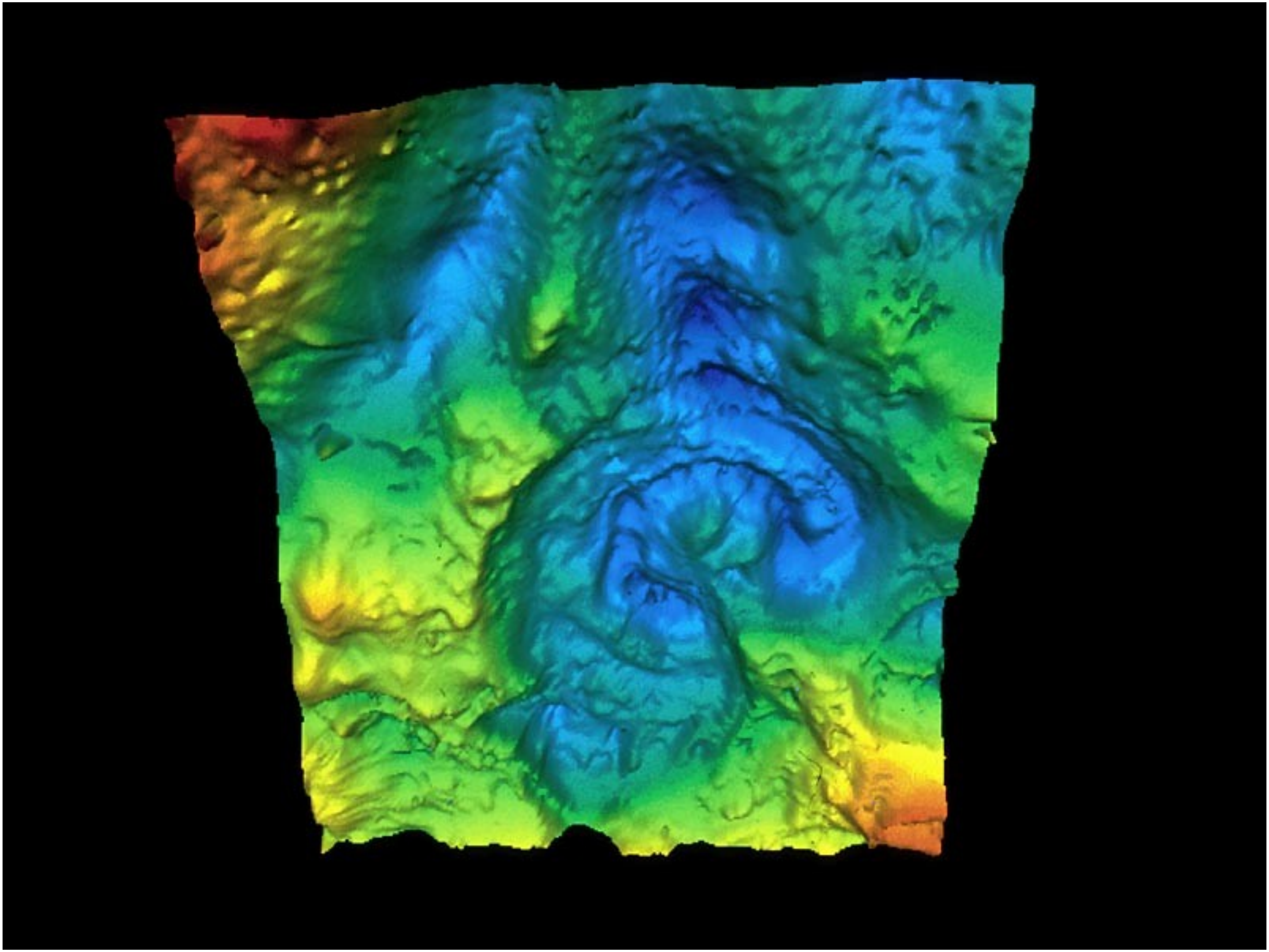
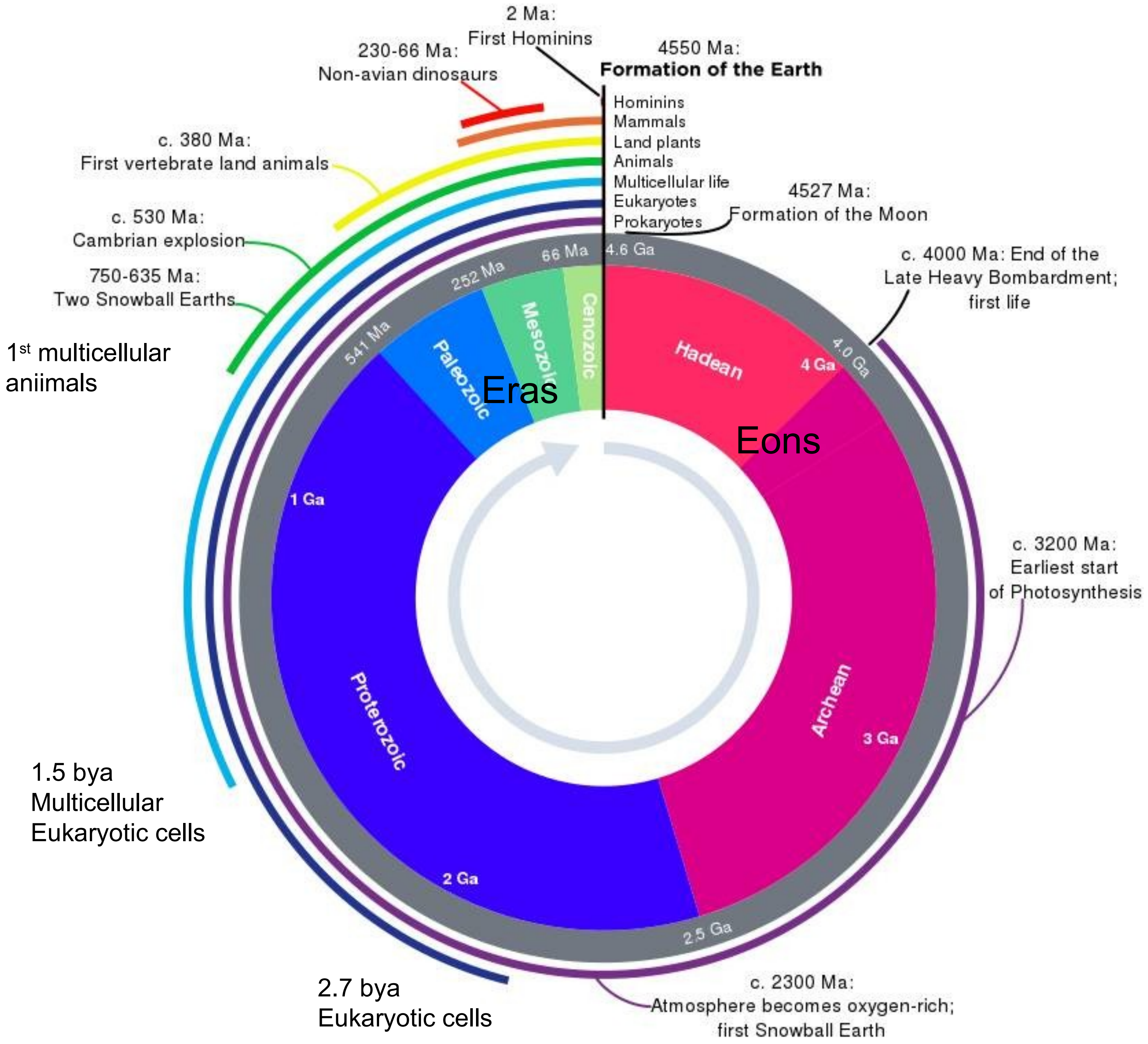
Chicxulub crater





1st multicellular
aniimals

Eras

Eons

1.5 bya
Multicellular
Eukaryotic cells

2.7 bya
Eukaryotic cells

By WoudloperDerivative work: Hardwigg - File:Geologic_clock.jpg, Public Domain, https://commons.wikimedia.org/w/index.php?curid=11926892

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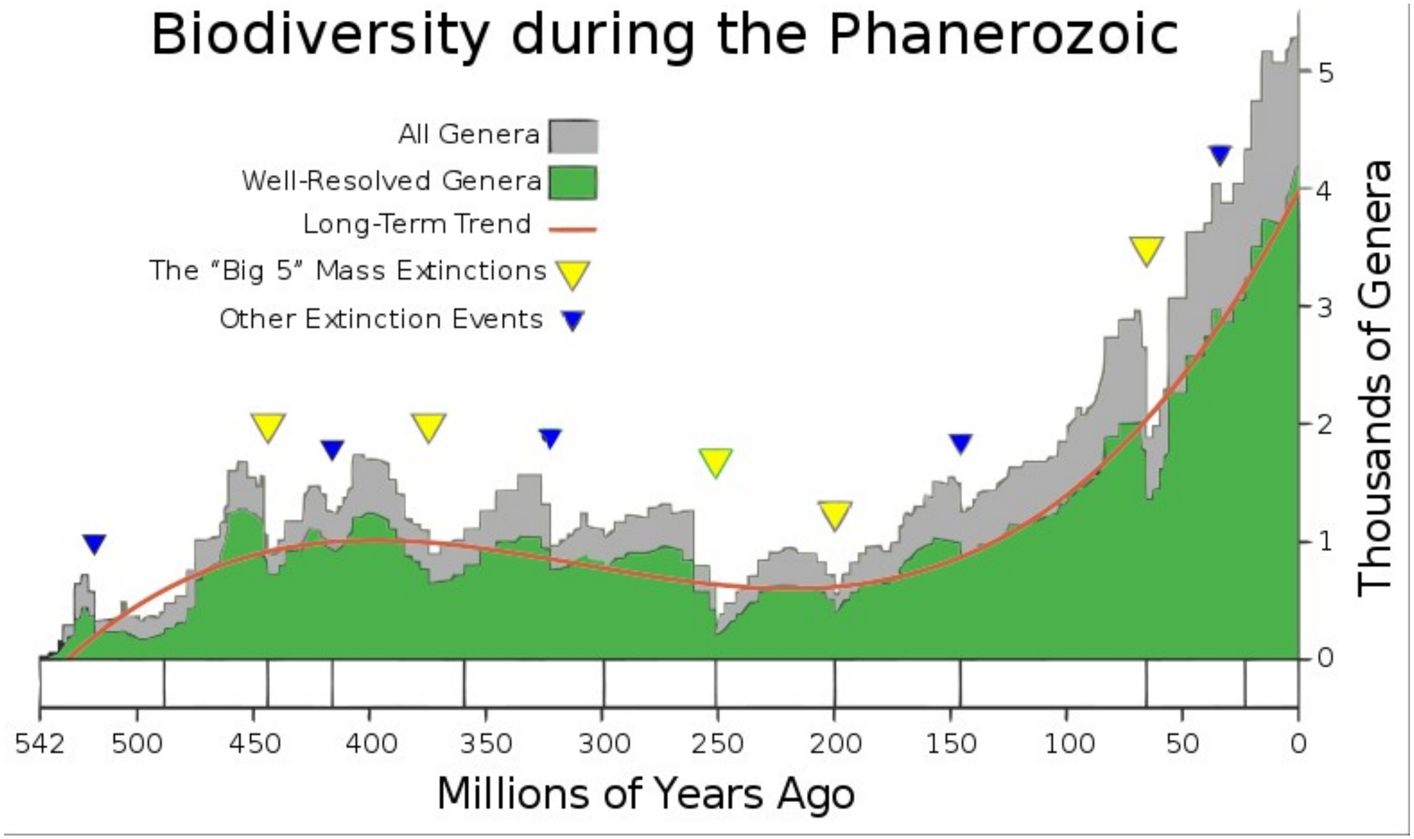
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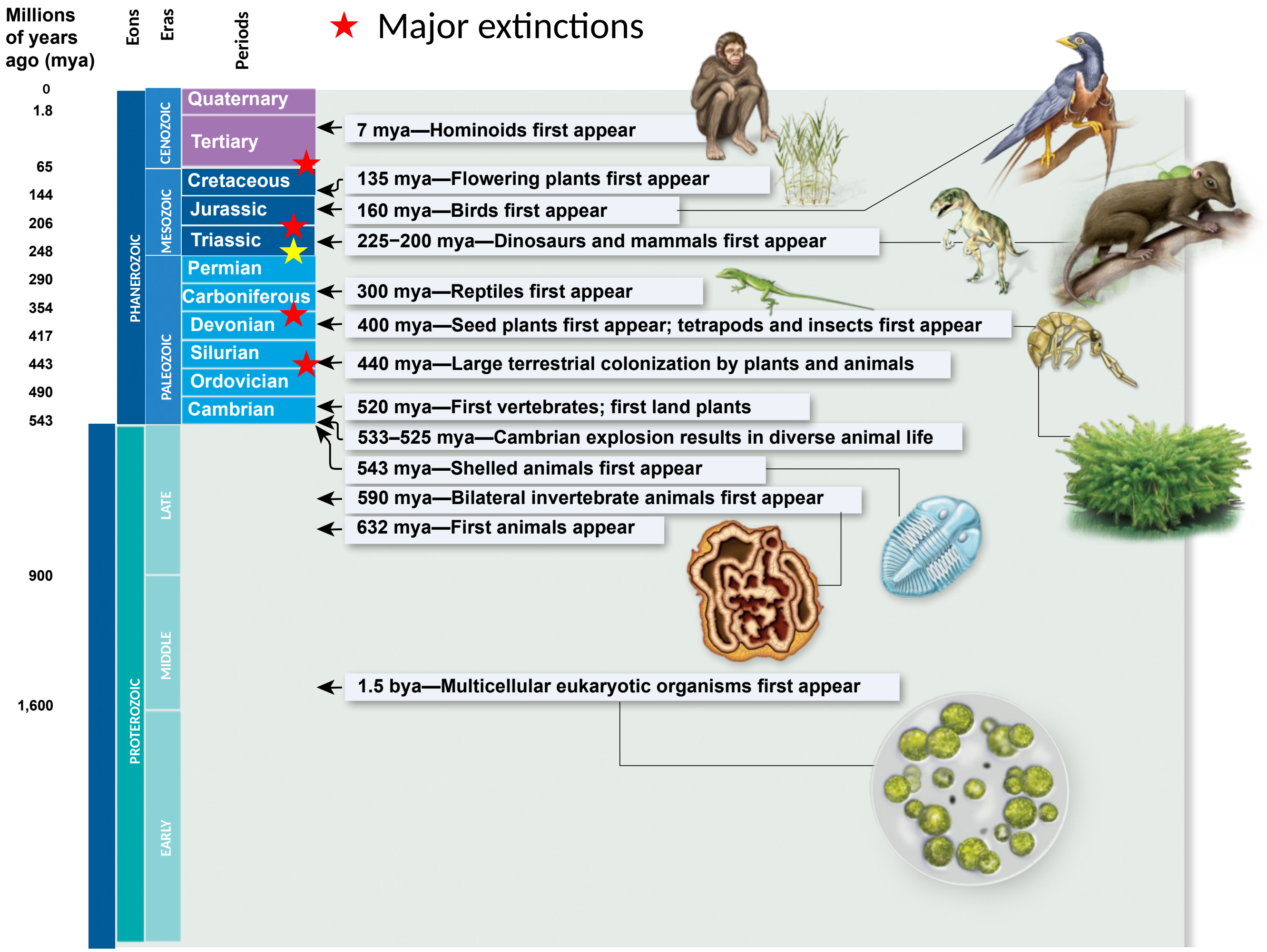

★ Major extinctions

Millions of years ago (mya)

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Eras

Periods

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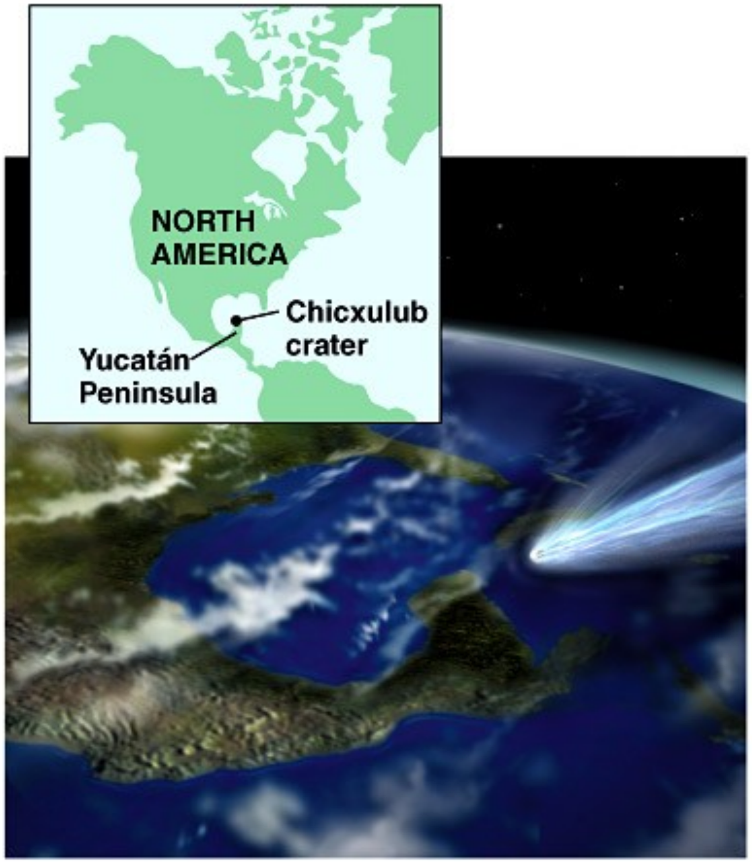

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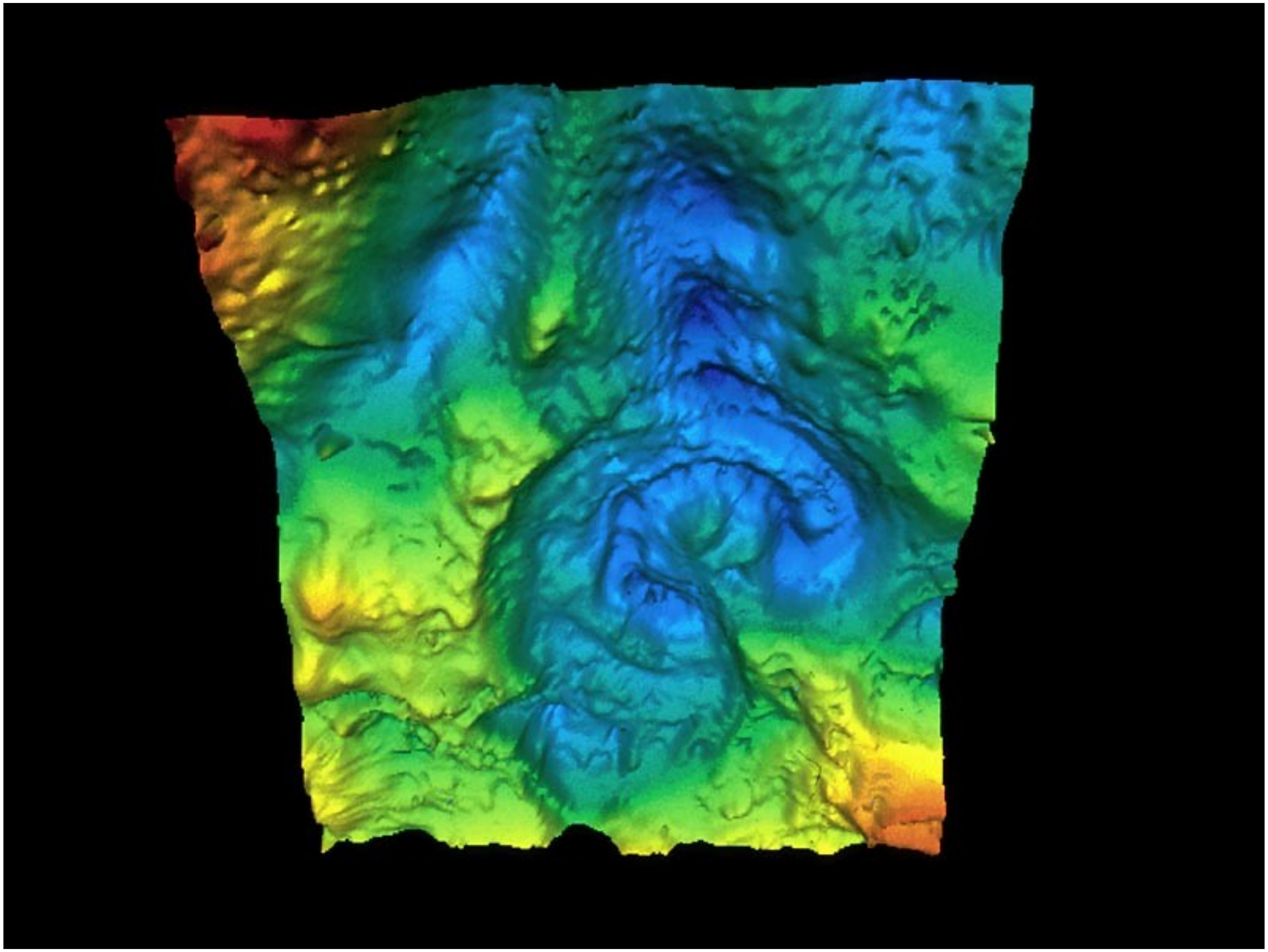
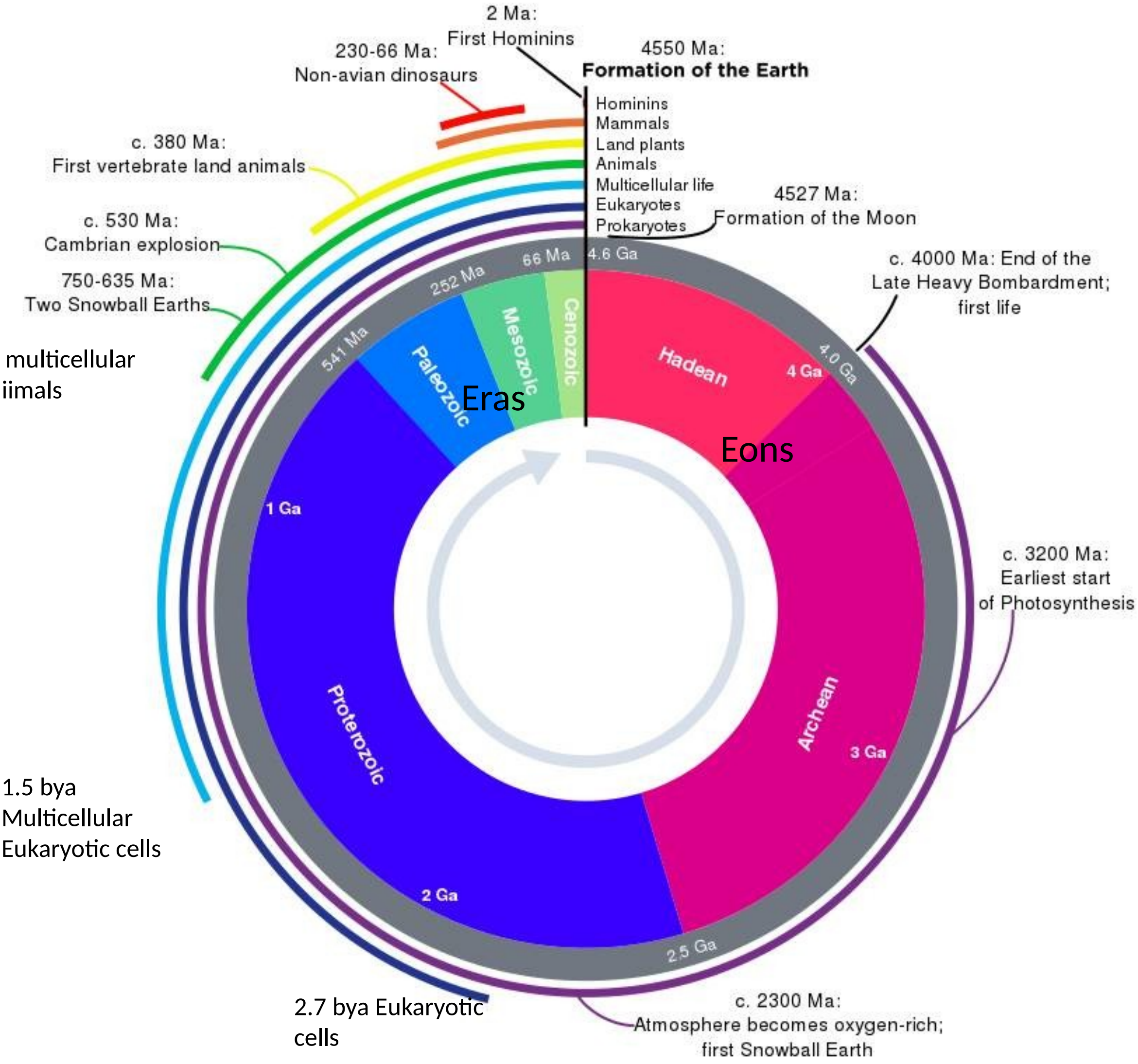
Chicxulub crater





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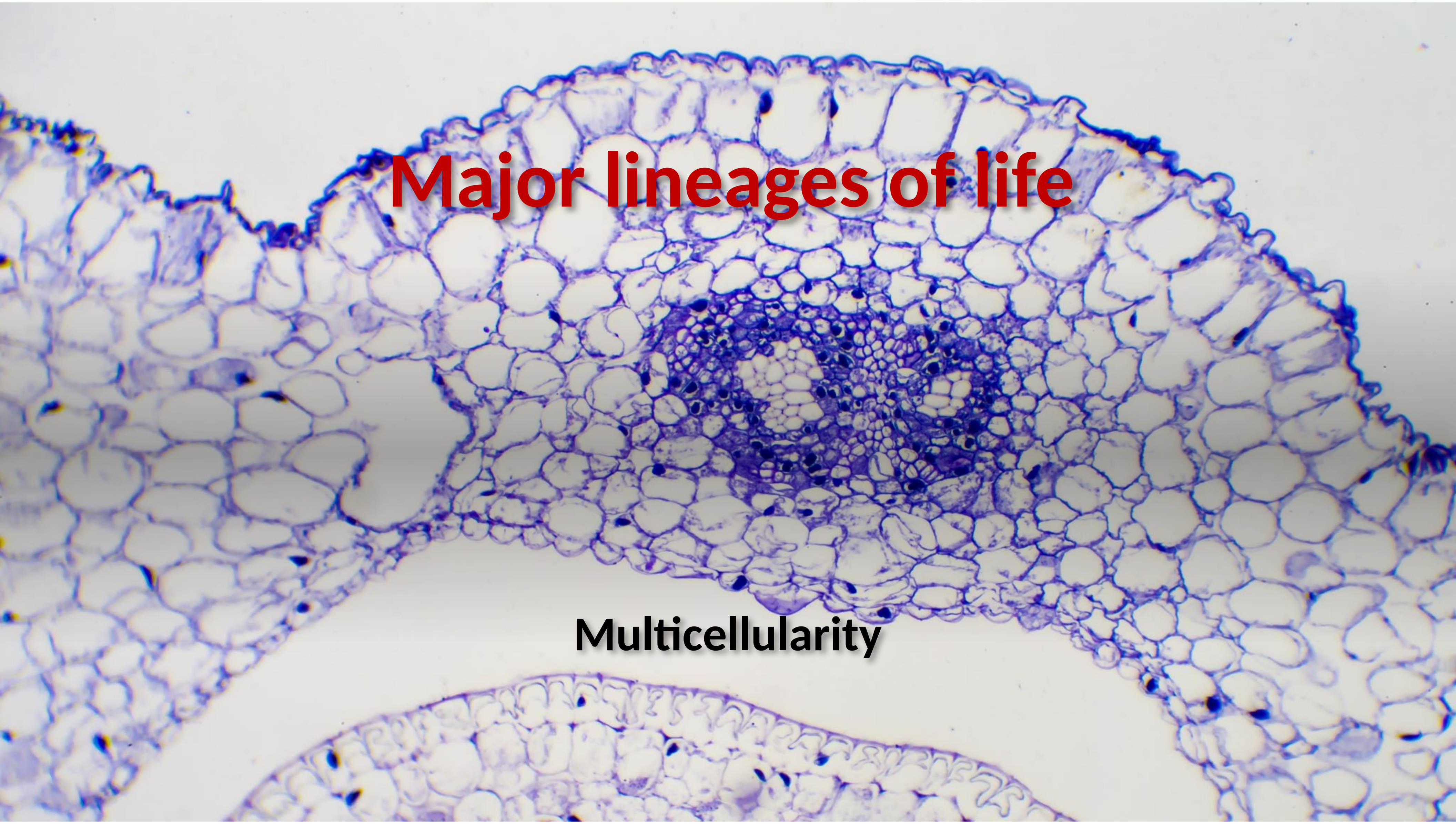
By WoudloperDerivative work: Hardwigg - File:Geologic_clock.jpg, Public Domain, https://commons.wikimedia.org/w/index.php?curid=11926892



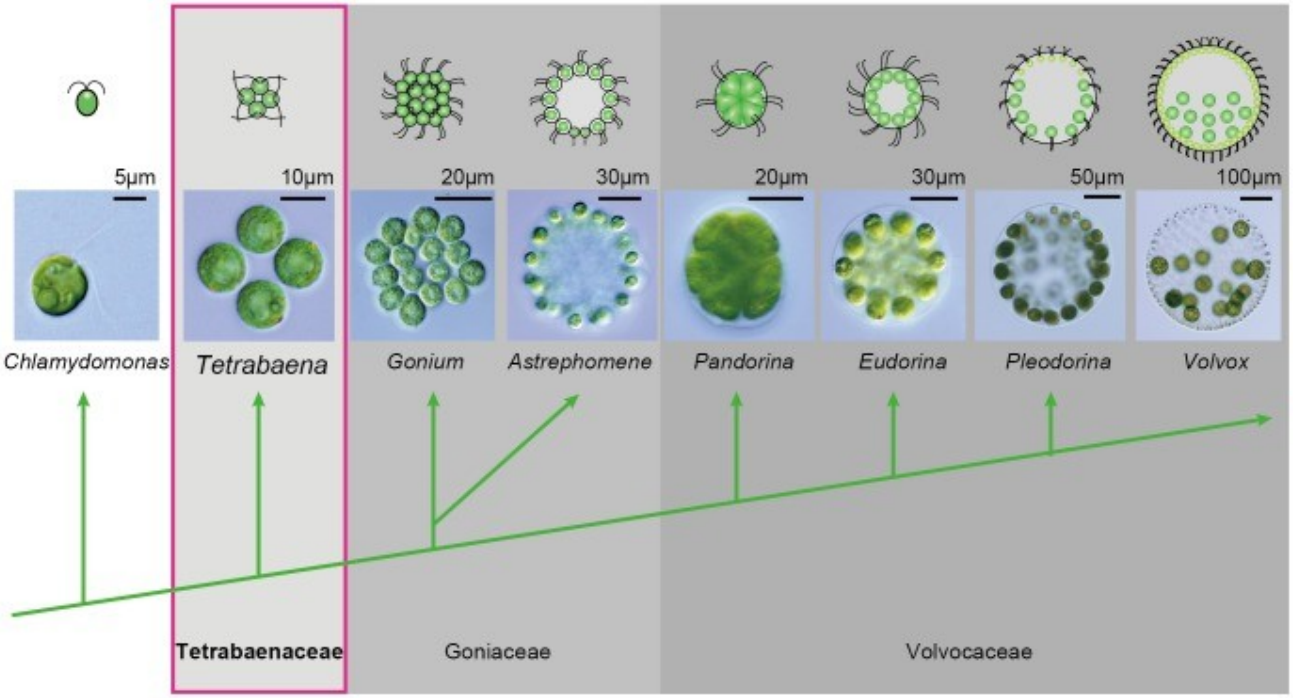
Major lineages of life

Multicellularity

Proterozoic Eon 2500-540mya

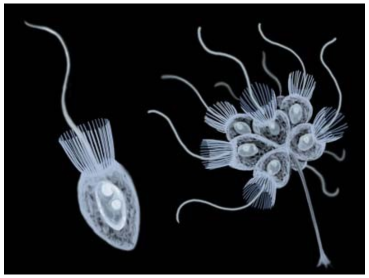
- **Oxygen build up 2.3bya**
- **Multicellular eukaryotes** arose 1.5 bya
- Two possible origins
  - ☐ Individuals formed a **colony**
  - ☐ Single cell **divided** and stayed stuck together
- **Contemporary Volvocine green algae** display variations in the degree of multicellularity

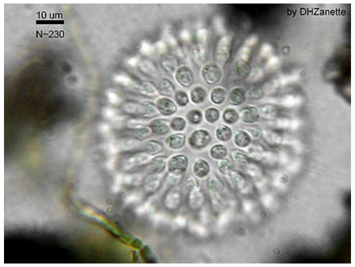
Volvocine green algae

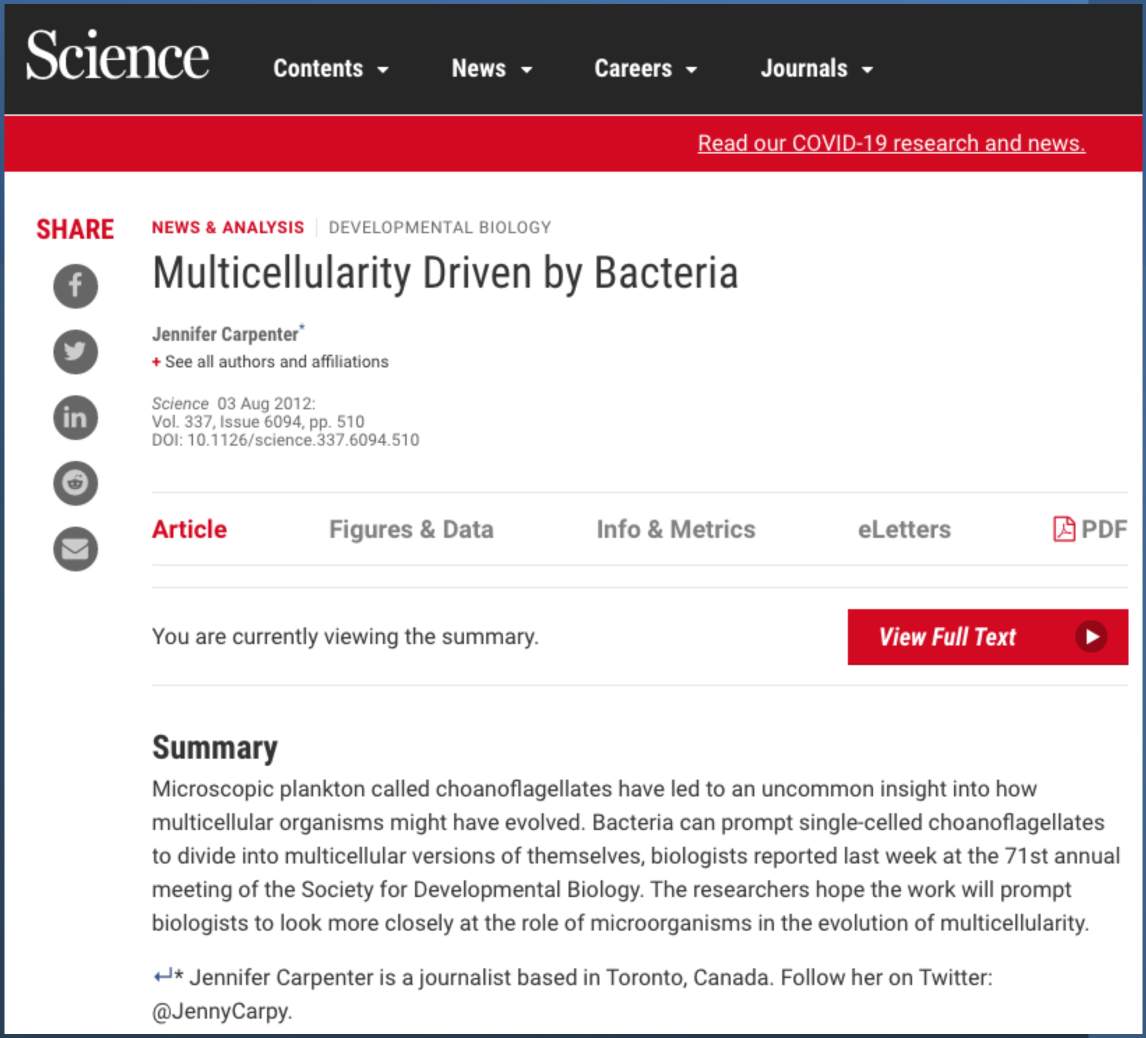


Multicellularity Driven by Bacteria August 2012 Science

Microscopic plankton called **choanoflagellates** have led to an uncommon insight into how multicellular organisms might have evolved. **Bacteria can prompt single-celled choanoflagellates to divide into multicellular versions of themselves**, biologists reported last week at the 71st annual meeting of the Society for Developmental Biology. The researchers hope the work will prompt biologists to look more closely at the role of microorganisms in the evolution of multicellularity. (Jennifer Carpenter, Science News)







NEWS & ANALYSIS | DEVELOPMENTAL BIOLOGY

Multicellularity Driven by Bacteria

Jennifer Carpenter[*]
+ See all authors and affiliations

Science 03 Aug 2012:
Vol. 337, Issue 6094, pp. 510
DOI: 10.1126/science.337.6094.510

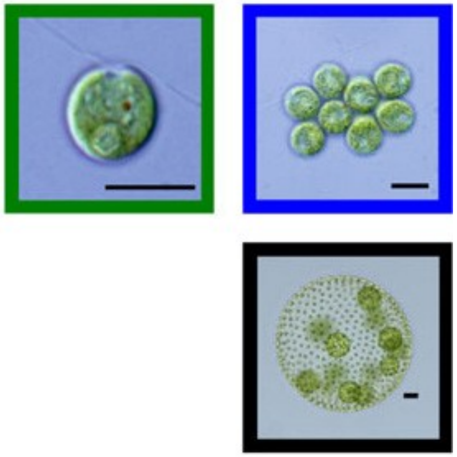
You are currently viewing the summary.

Summary

Microscopic plankton called choanoflagellates have led to an uncommon insight into how multicellular organisms might have evolved. Bacteria can prompt single-celled choanoflagellates to divide into multicellular versions of themselves, biologists reported last week at the 71st annual meeting of the Society for Developmental Biology. The researchers hope the work will prompt biologists to look more closely at the role of microorganisms in the evolution of multicellularity.

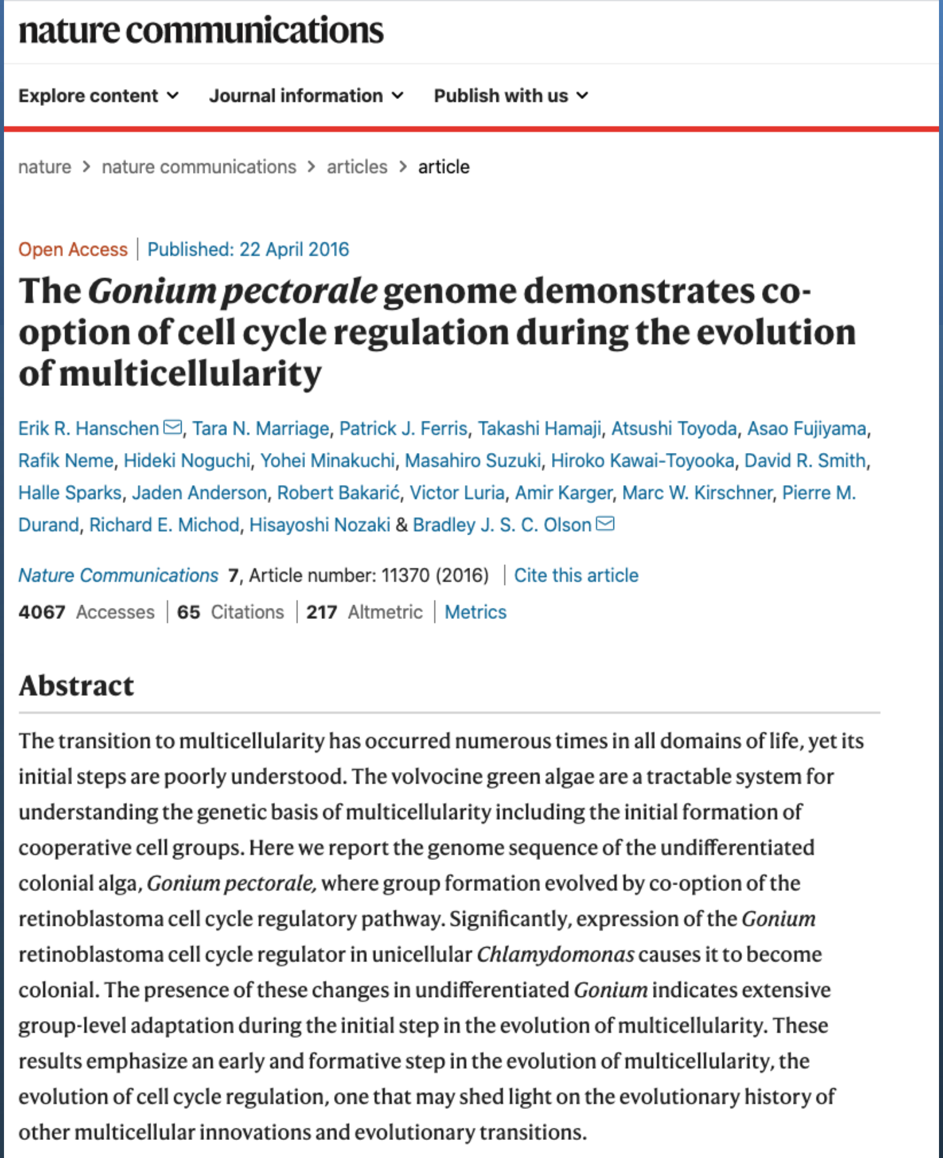
↵* Jennifer Carpenter is a journalist based in Toronto, Canada. Follow her on Twitter: @JennyCarpy.

Unicellular to Multicellular with one gene change



Chlamydomonas, Gonium, Volvox

- To simplify such genomic analyses, researchers led by Erik Hanschen at the University of Arizona and Bradley Olson at Kansas State University compared the genomic sequences of three species of green algae in the order Volvocales in order to pinpoint the gene changes underlying the evolution of multicellularity. They recently published their results in *Nature Communications*. (Hanschen et al, Apr 22, 2016; 7:11370)
- "Rather than the situation where hundreds of genes have to evolve simultaneously, **it's a very subtle change in one gene that causes a reprograming of the cell cycle**," Olson said in a press release. (Patrick CH Lo 05/19/2016)
- Cell cycle regulator gene is responsible



Open Access | Published: 22 April 2016

The *Gonium pectorale* genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity

Erik R. Hanschen, Tara N. Marriage, Patrick J. Ferris, Takashi Hamaji, Atsushi Toyoda, Asao Fujiyama, Rafik Neme, Hideki Noguchi, Yohei Minakuchi, Masahiro Suzuki, Hiroko Kawai-Toyooka, David R. Smith, Halle Sparks, Jaden Anderson, Robert Bakarić, Victor Luria, Amir Karger, Marc W. Kirschner, Pierre M. Durand, Richard E. Michod, Hisayoshi Nozaki & Bradley J. S. C. Olson

Nature Communications **7**, Article number: 11370 (2016) | Cite this article

4067 Accesses | **65** Citations | **217** Altmetric | Metrics

Abstract

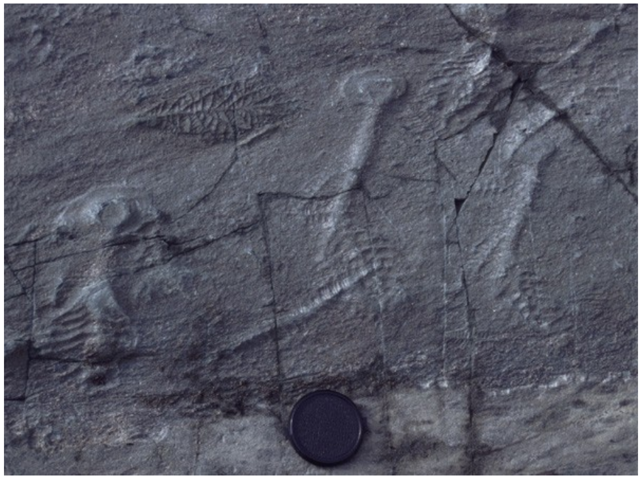
The transition to multicellularity has occurred numerous times in all domains of life, yet its initial steps are poorly understood. The volvocine green algae are a tractable system for understanding the genetic basis of multicellularity including the initial formation of cooperative cell groups. Here we report the genome sequence of the undifferentiated colonial alga, *Gonium pectorale,* where group formation evolved by co-option of the retinoblastoma cell cycle regulatory pathway. Significantly, expression of the *Gonium* retinoblastoma cell cycle regulator in unicellular *Chlamydomonas* causes it to become colonial. The presence of these changes in undifferentiated *Gonium* indicates extensive group-level adaptation during the initial step in the evolution of multicellularity. These results emphasize an early and formative step in the evolution of multicellularity, the evolution of cell cycle regulation, one that may shed light on the evolutionary history of other multicellular innovations and evolutionary transitions.

Proterozoic Eon summary (2.5 bya – 540 mya)

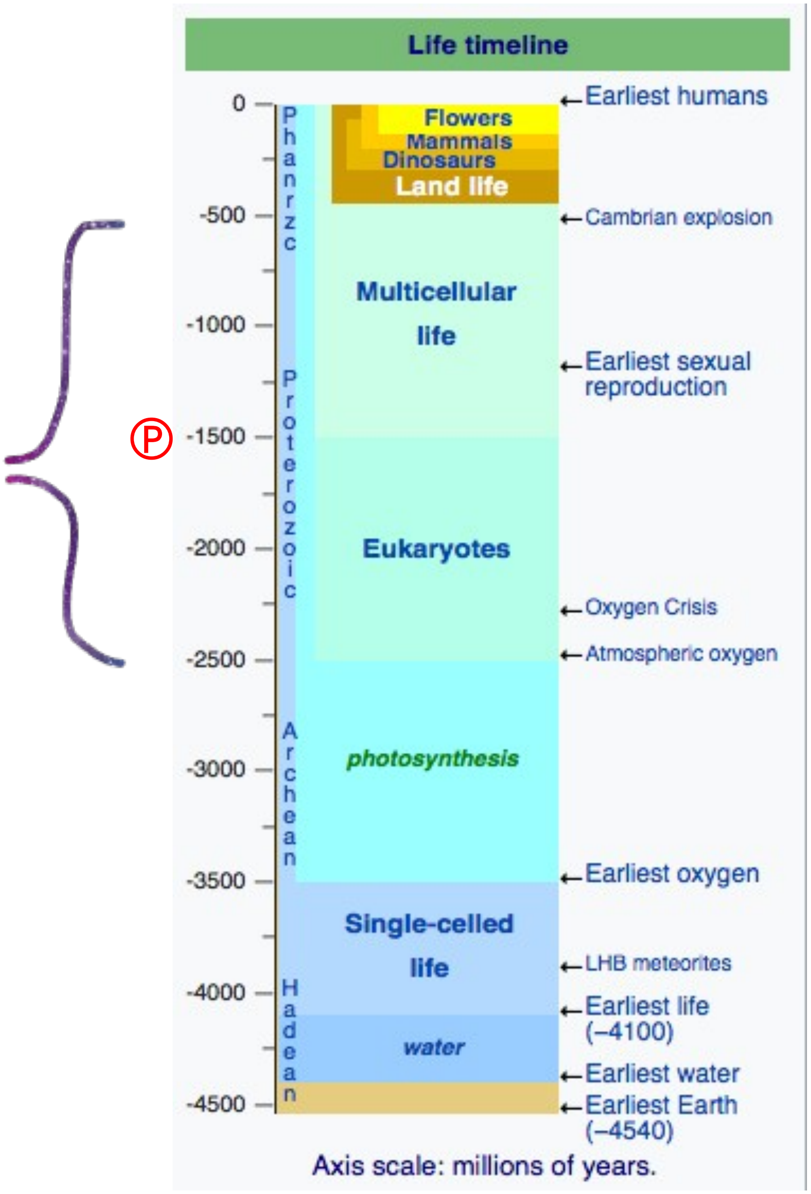
(part of Pre-Cambrian)

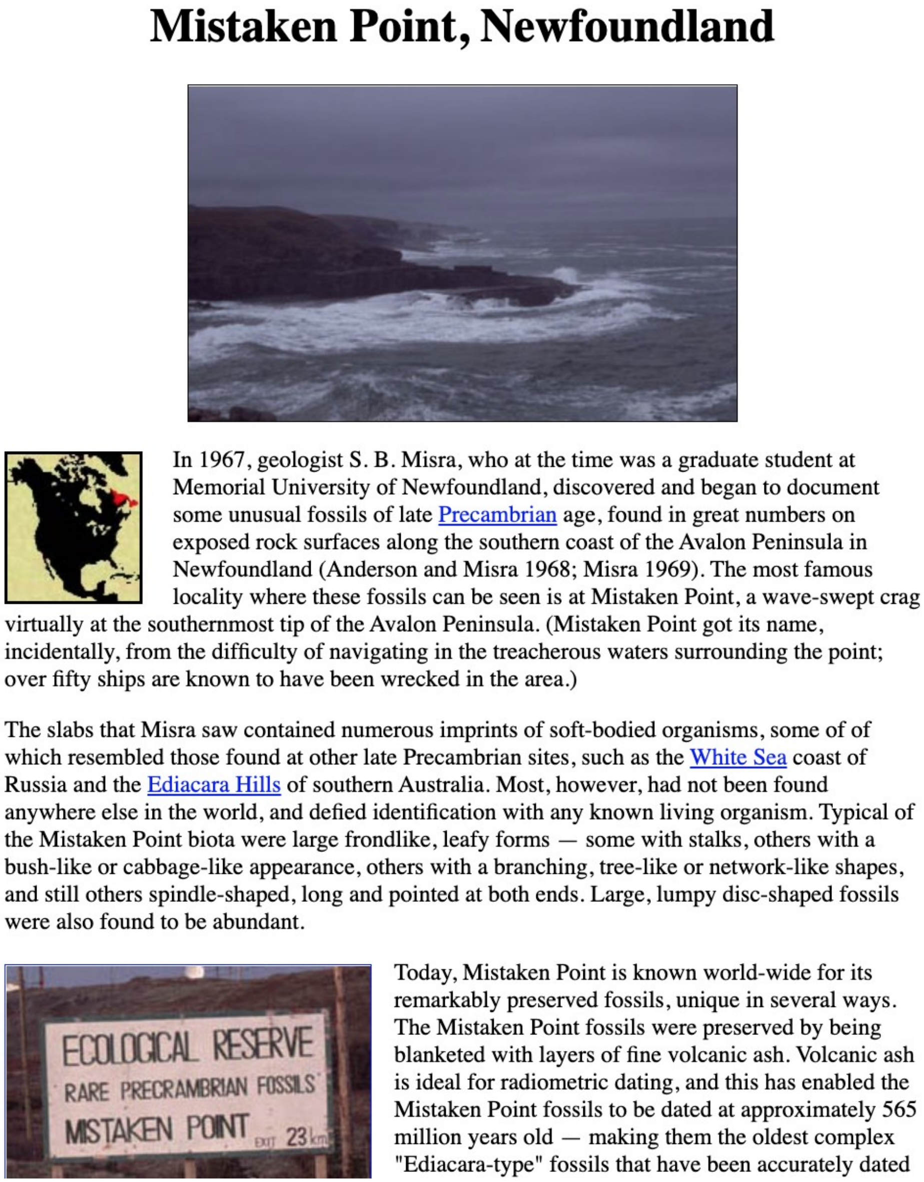
- **1st continents appeared (3 bya)**
- **1st eukaryotic cells appear (2.7 bya)**
- **Oxygen builds up to toxic levels (2.3 bya)**
- **Multicellular life** emerged toward the end of the Proterozoic Eon (**1.5 to 0.5 bya**)
  - Soft bodied, radial or no symmetry
- 1st animals lacked bones (invertebrates) (632mya)
  - ❑ **Bilateral symmetry evolved** (590mya) **-** facilitates movement
- **1st shelled animal**s (543 mya)
- Cambrian explosion (540 mya)

http://www.ucmp.berkeley.edu/vendian/mistaken.html



Proterozoic Eon





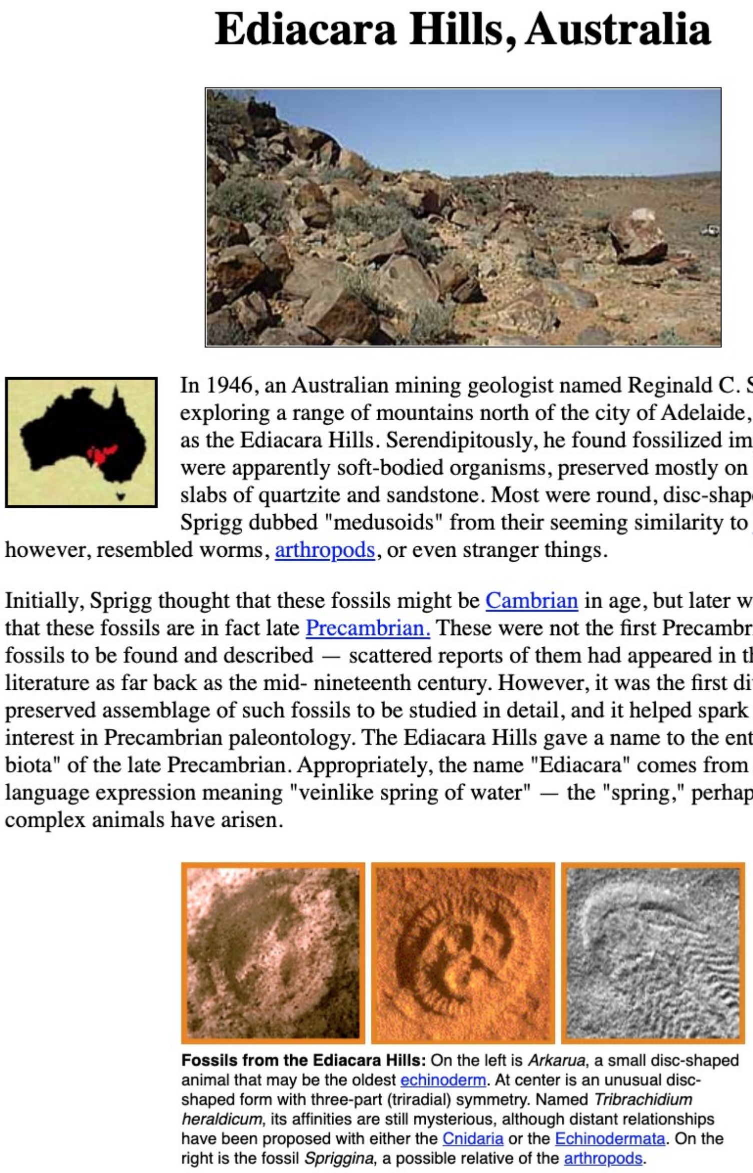
Mistaken Point, Newfoundland

In 1967, geologist S. B. Misra, who at the time was a graduate student at Memorial University of Newfoundland, discovered and began to document some unusual fossils of late Precambrian age, found in great numbers on exposed rock surfaces along the southern coast of the Avalon Peninsula in Newfoundland (Anderson and Misra 1968; Misra 1969). The most famous locality where these fossils can be seen is at Mistaken Point, a wave-swept crag virtually at the southernmost tip of the Avalon Peninsula. (Mistaken Point got its name, incidentally, from the difficulty of navigating in the treacherous waters surrounding the point; over fifty ships are known to have been wrecked in the area.)

The slabs that Misra saw contained numerous imprints of soft-bodied organisms, some of of which resembled those found at other late Precambrian sites, such as the White Sea coast of Russia and the Ediacara Hills of southern Australia. Most, however, had not been found anywhere else in the world, and defied identification with any known living organism. Typical of the Mistaken Point biota were large frondlike, leafy forms — some with stalks, others with a bush-like or cabbage-like appearance, others with a branching, tree-like or network-like shapes, and still others spindle-shaped, long and pointed at both ends. Large, lumpy disc-shaped fossils were also found to be abundant.

Today, Mistaken Point is known world-wide for its remarkably preserved fossils, unique in several ways. The Mistaken Point fossils were preserved by being blanketed with layers of fine volcanic ash. Volcanic ash is ideal for radiometric dating, and this has enabled the Mistaken Point fossils to be dated at approximately 565 million years old — making them the oldest complex "Ediacara-type" fossils that have been accurately dated

Precambrian soft-bodied organism impressions



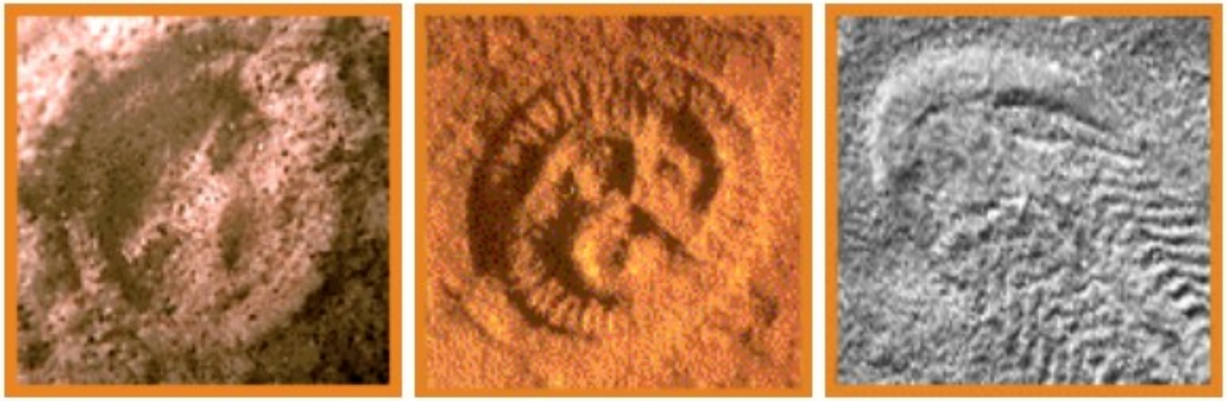
Ediacara Hills, Australia

In 1946, an Australian mining geologist named Reginald C. Sprigg was exploring a range of mountains north of the city of Adelaide, Australia, known as the Ediacara Hills. Serendipitously, he found fossilized imprints of what were apparently soft-bodied organisms, preserved mostly on the undersides of slabs of quartzite and sandstone. Most were round, disc-shaped forms that Sprigg dubbed "medusoids" from their seeming similarity to jellyfish. Others, however, resembled worms, arthropods, or even stranger things.

Initially, Sprigg thought that these fossils might be Cambrian in age, but later work established that these fossils are in fact late Precambrian. These were not the first Precambrian soft- bodied fossils to be found and described — scattered reports of them had appeared in the scientific literature as far back as the mid- nineteenth century. However, it was the first diverse and well-preserved assemblage of such fossils to be studied in detail, and it helped spark a surge of interest in Precambrian paleontology. The Ediacara Hills gave a name to the entire "Ediacara biota" of the late Precambrian. Appropriately, the name "Ediacara" comes from an Aboriginal language expression meaning "veinlike spring of water" — the "spring," perhaps, from which complex animals have arisen.

Fossils from the Ediacara Hills: On the left is *Arkarua*, a small disc-shaped animal that may be the oldest echinoderm. At center is an unusual disc-shaped form with three-part (triradial) symmetry. Named *Tribrachidium heraldicum*, its affinities are still mysterious, although distant relationships have been proposed with either the Cnidaria or the Echinodermata. On the right is the fossil *Spriggina*, a possible relative of the arthropods.

Precambrian soft-bodied organism impressions including jellyfish-like, worm-like, even arthropod-like



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The Winter Coast of Russia

During the summers of 1993 and 1994, UC graduate students Ben Waggoner and Allen Collins visited the Winter Coast Region of Russia to examine rocks containing the richest Vendian fossils in the world. During the summer of 1993, these two researchers were joined by professor Jere Lipps and a team of American volunteers, in conjunction with Dr. Mikhail A. Fedonkin and a team of Russian scientists from the Paleontological Institute of the Russian Academy of Sciences in Moscow. Ben and Allen returned during the summer of 1994 with three Russian scientists to carry out further research.

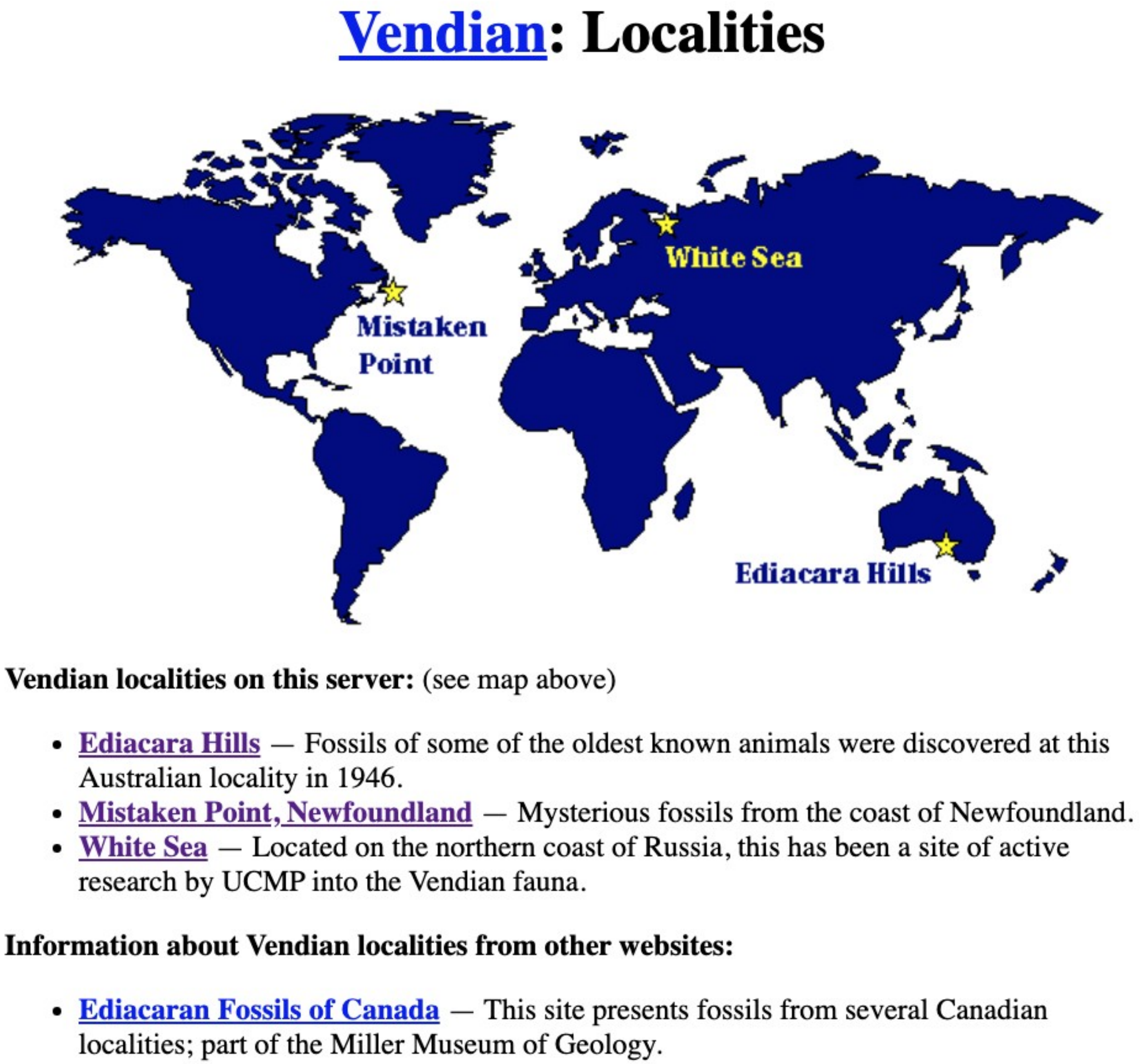
In order to get to the Winter Coast region which is approximately 65 degrees north latitude, these intrepid researchers travelled 24 hours north by train out of Moscow to the city of Archangelsk. Moscow is a city which is already as far north as Edmonton, Alberta in Canada. Archangelsk is a city with over a million people. From there, the trip continued by ship. During 1993, the ship ride was nine hours long, but Ben and Allen had it considerably better in 1994 when they travelled by hover craft. That trip took less than three hours.

The object of the visit was to find fossils, but what do you think it was like to actually be there?

1. If you were there, you would have to make camp.
2. You would have to hike to, and up, steep cliffs.
3. And, you would have to look in the cliffs for your fossils.

UCMP Special Exhibit: Vendian Animals
Ben Waggoner collected a number of interesting fossils while visiting the White Sea. You can learn about these in his exhibit.

In the
Proterozoic:
Vendian=
Ediacaran



Vendian: Localities

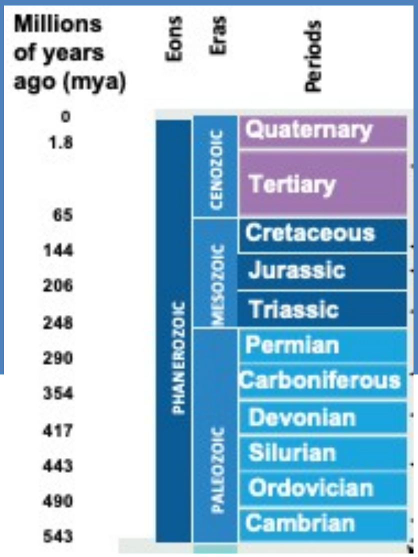
Vendian localities on this server: (see map above)

- Ediacara Hills — Fossils of some of the oldest known animals were discovered at this Australian locality in 1946.
- Mistaken Point, Newfoundland — Mysterious fossils from the coast of Newfoundland.
- White Sea — Located on the northern coast of Russia, this has been a site of active research by UCMP into the Vendian fauna.

Information about Vendian localities from other websites:

- Ediacaran Fossils of Canada — This site presents fossils from several Canadian localities; part of the Miller Museum of Geology.

Phanerozoic Eon (lots of fossils)



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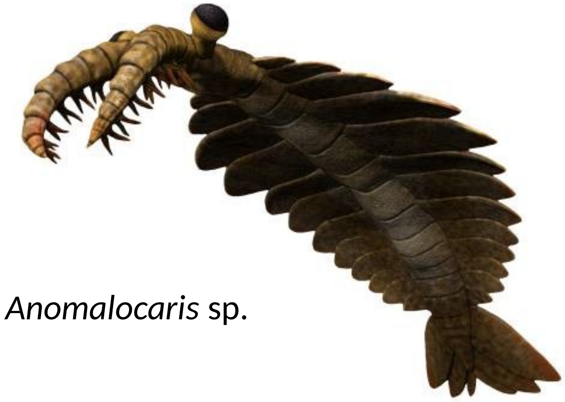
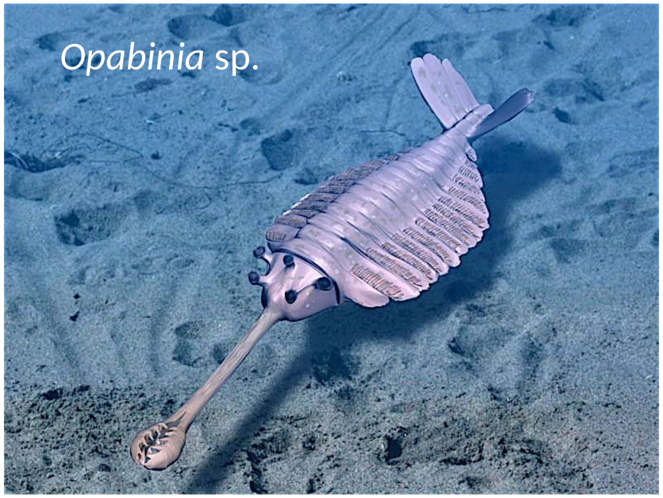
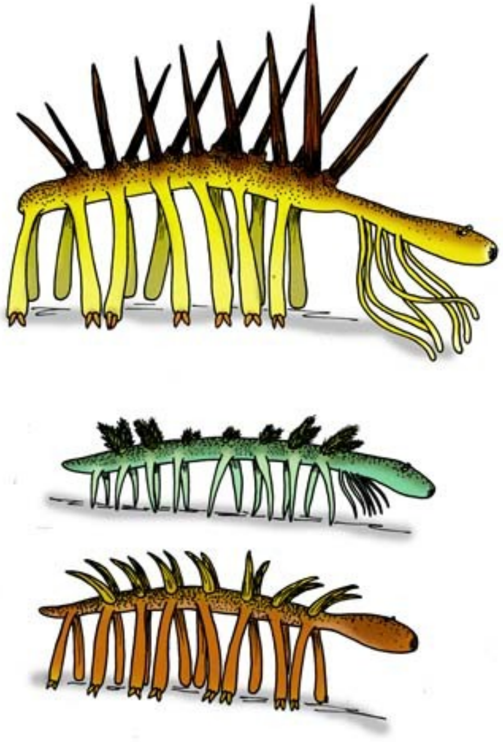
490			Cambrian
543			

- Proliferation of multicellular eukaryotic life extensive (543 mya to today)
- **Paleozoic Era** 543-250 mya
- **Mesozoic Era** 250-65 mya
- **Cenozoic Era** 65 mya to present

Fun organisms from Cambrian explosion


Anomalocaris sp.


Opabinia sp.


Hallucinogenia sp.

Cambrian Explosion Crash Course

Phanerozoic Eon – **Paleozoic Era (540-250mya)**

540mya

250mya

- **Cambrian period:** warm, wet, **Cambrian explosion**, Burgess Shale fossils include soft bodies
- **Ordovician period:** warm, wet, trilobites, jawless fishes (**1st vertebrates**), mollusks, corals….then glaciers=mass extinction
- **Silurian period:** coral reefs, more fishes, plant & animal **land colonization**, 1st **vascular plants, 1st arachnids**
- **Devonian period:** tall plants, **1st seed plants-gymnosperms**, fern forests, **1st insects**, **1st tetrapods**, Age of Fishes, some extinctions
- **Carboniferous period:** coal (compressed layers rotting vegetation), 1st flying insects, 1st **amniotic egg and reptiles**
- **Permian period:** Pangaea….then largest mass extinction in history of life on Earth = 90-95% marine sp. + many terrestrial species (glaciers or volcanoes)

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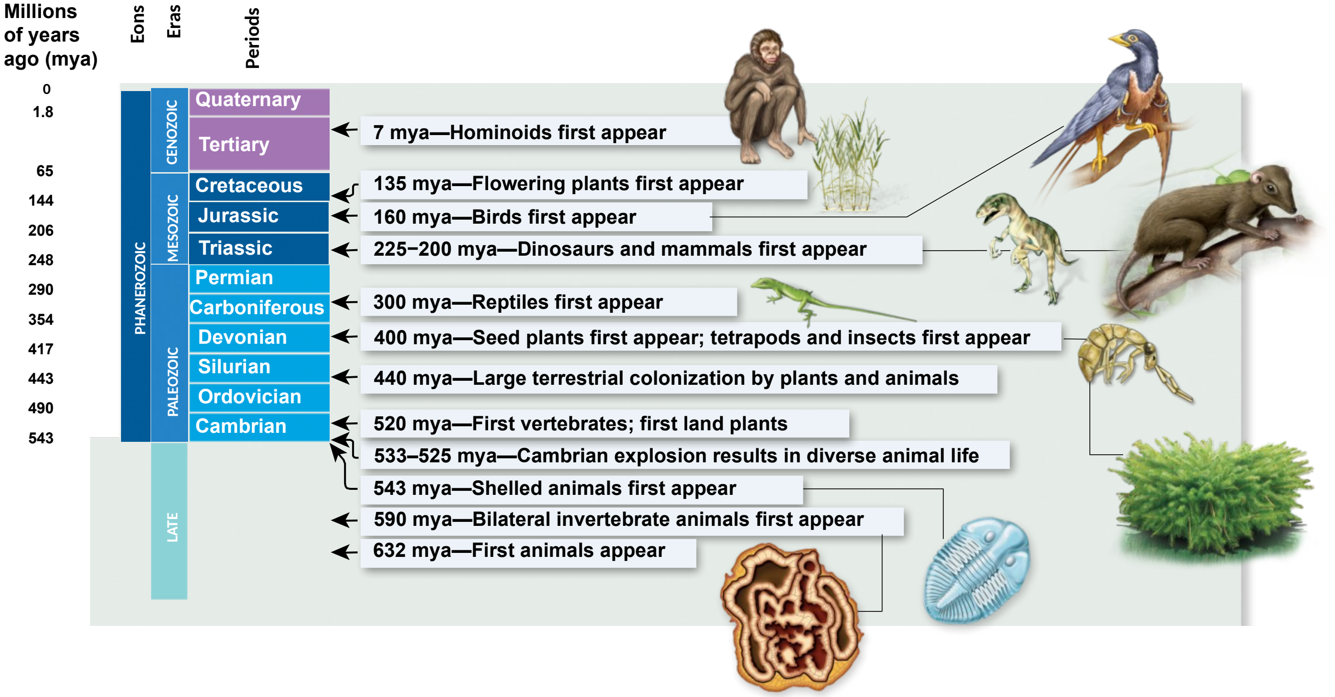


7 mya—Hominoids first appear

135 mya—Flowering plants first appear

160 mya—Birds first appear

225–200 mya—Dinosaurs and mammals first appear

300 mya—Reptiles first appear

400 mya—Seed plants first appear; tetrapods and insects first appear

440 mya—Large terrestrial colonization by plants and animals

520 mya—First vertebrates; first land plants

533–525 mya—Cambrian explosion results in diverse animal life

543 mya—Shelled animals first appear

590 mya—Bilateral invertebrate animals first appear

632 mya—First animals appear

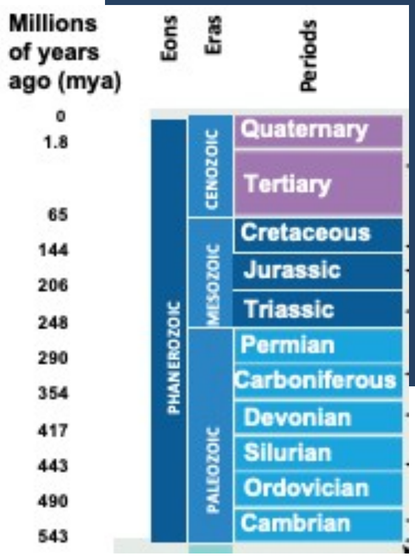
End Permian, 251 million years ago, 96% of species lost

- Known as “the great dying”, this was by far the worst extinction event ever seen; it nearly ended life on Earth.

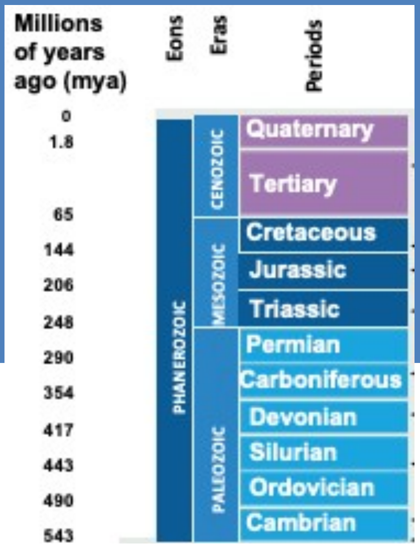
- What caused it? A perfect storm of natural catastrophes.

1. A cataclysmic eruption near Siberia blasted CO2 into the atmosphere.
2. Methanogenic bacteria responded by belching out methane, a potent greenhouse gas.
3. Global temperatures surged while oceans acidified and stagnated, belching poisonous hydrogen sulfide.

- “It set life back 300 million years,” says Schmidt.



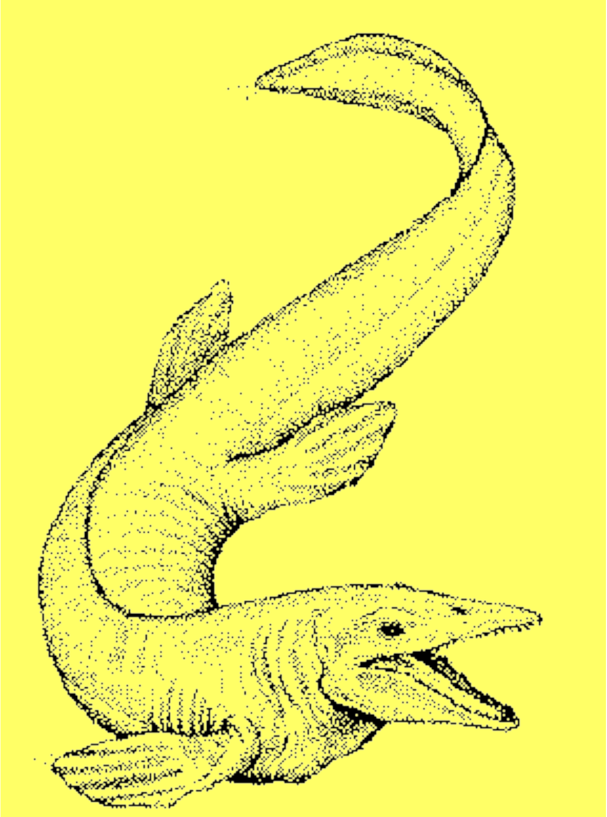
Phanerozoic Eon – Mesozoic Era (250-65mya)



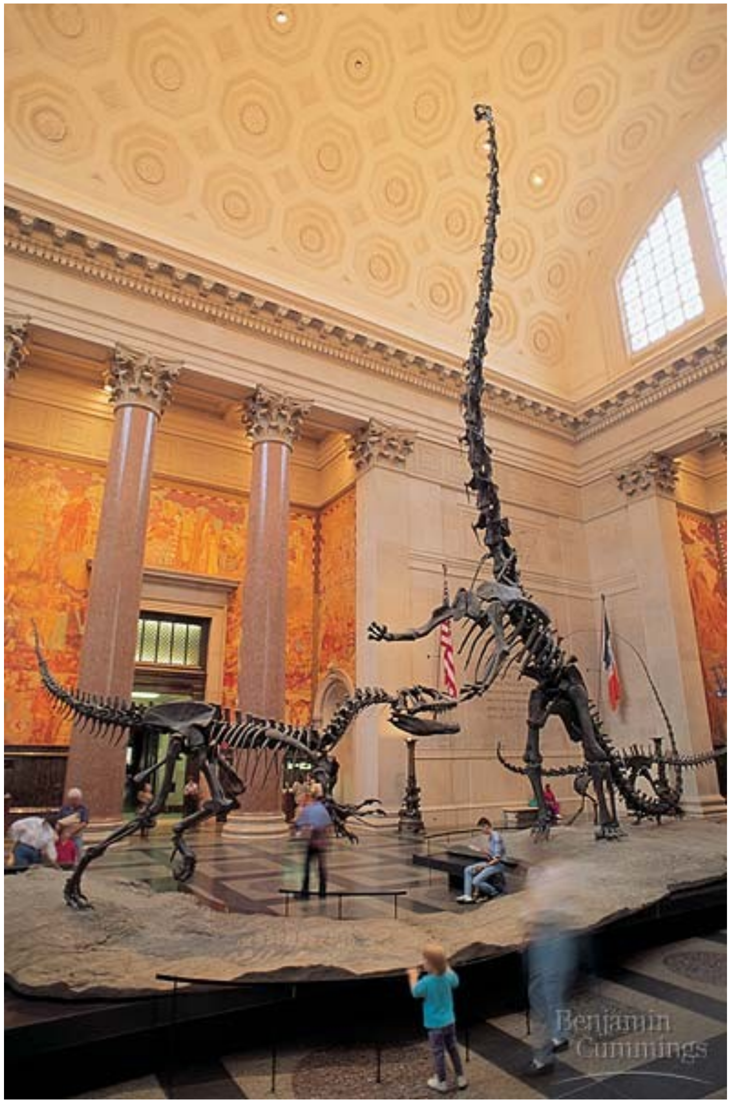
Millions of years ago (mya)	Eons	Eras	Periods
0	PHANEROZOIC	CENOZOIC	Quaternary
1.8			Tertiary
65		MESOZOIC	Cretaceous
144			Jurassic
206			Triassic
248		PALEOZOIC	Permian
290			Carboniferous
354			Devonian
417			Silurian
443			Ordovician
490			Cambrian
543			

- Permian extinction marks boundary between Paleozoic and Mesozoic eras
- **The Age of Dinosaurs**
- Consistently hot climate, dry terrestrial environments, little if any ice at poles

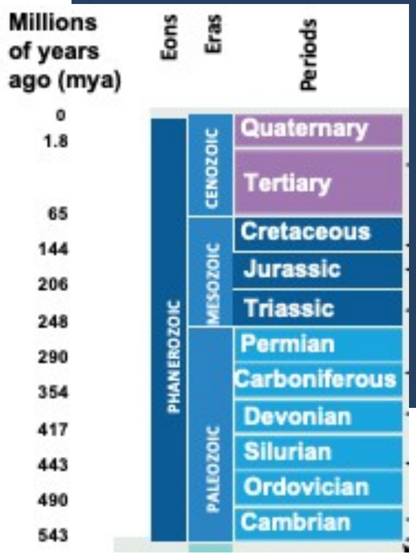
Dinosaur or similar fossils – first named by Cuvier (1808) [*Mosasaurus*, a marine reptile]



Barosaurus

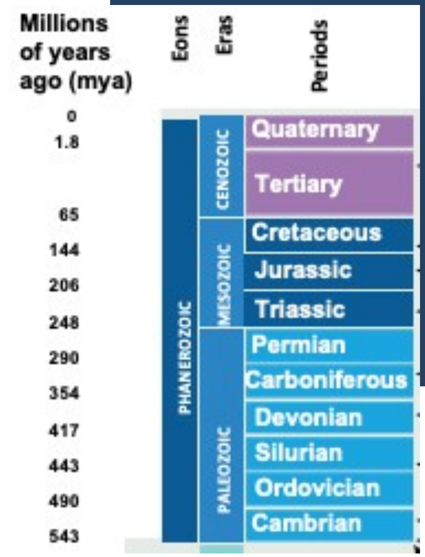


Phanerozoic Eon – Mesozoic Era – Triassic Period



- 248-206 mya
- Reptiles plentiful
- First **dinosaurs**
- First **true mammals**
- Gymnosperms dominant land plants
- Volcanic eruptions led to global warming and mass extinctions near the end

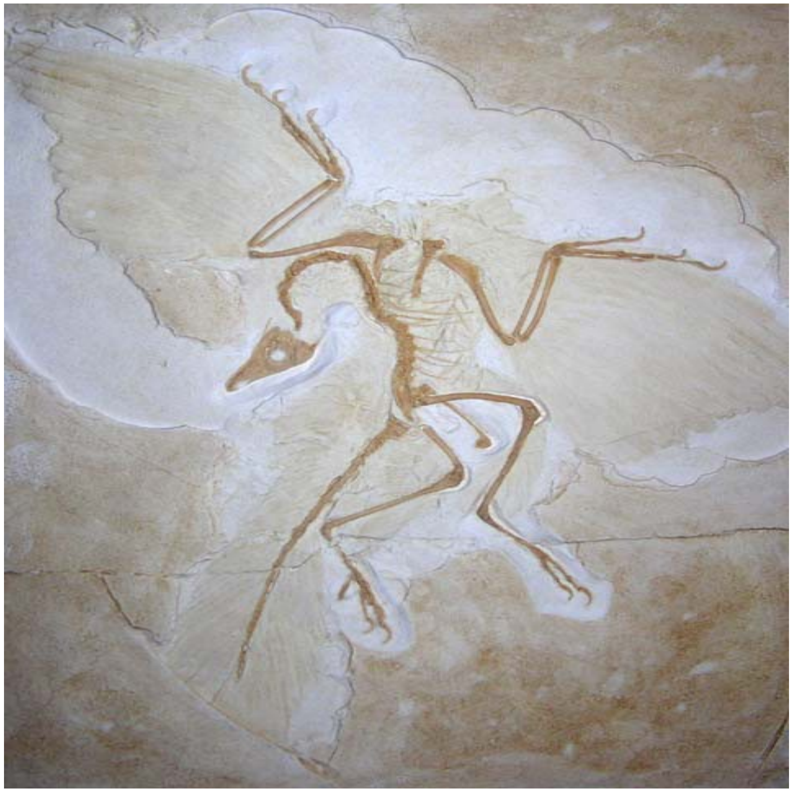
Phanerozoic Eon – Mesozoic Era – Jurassic Period



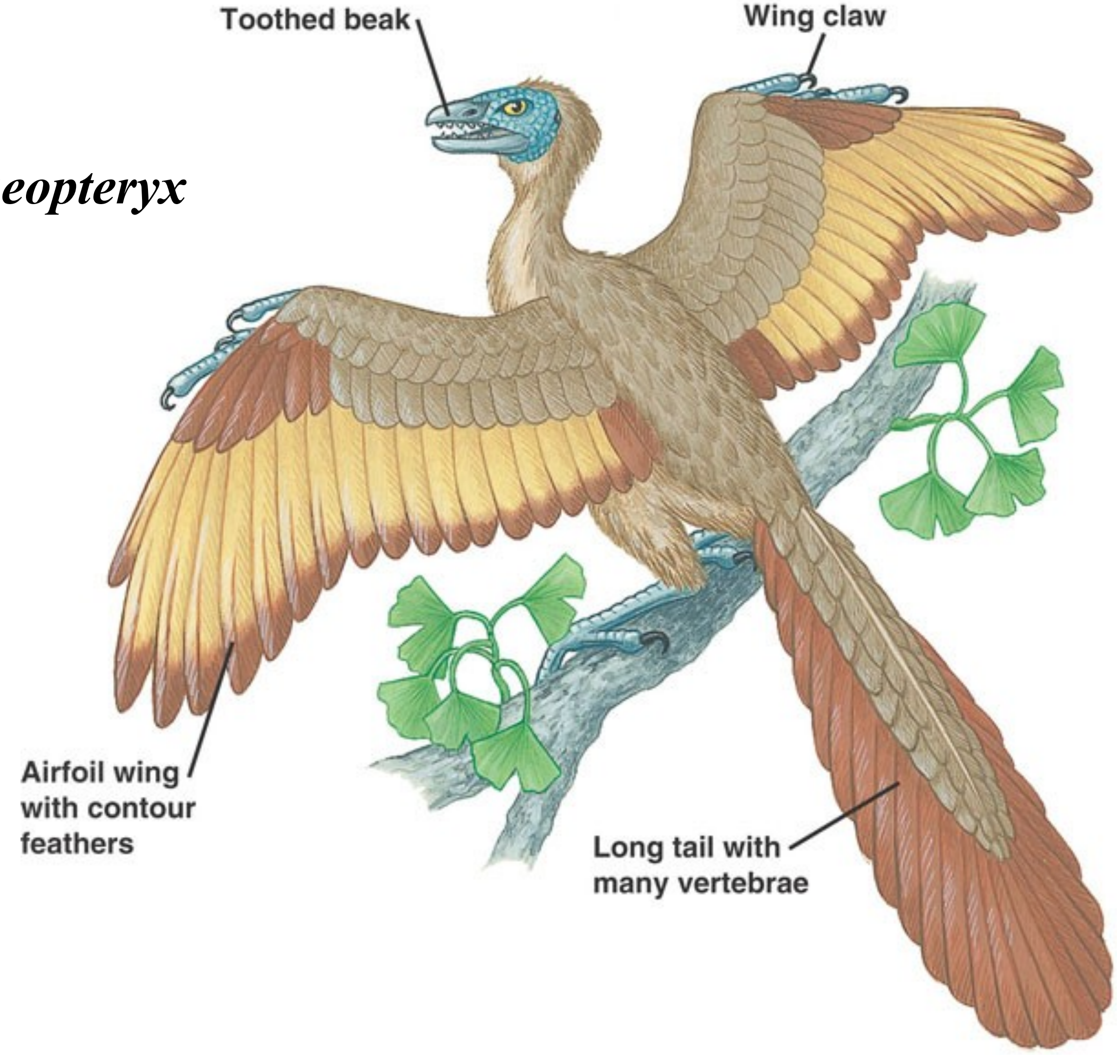
Millions of years ago (mya)	Eons	Eras	Periods
0			
1.8	PHANEROZOIC	CENOZOIC	Quaternary
65			Tertiary
144		MESOZOIC	Cretaceous
206			Jurassic
248			Triassic
290		PALEOZOIC	Permian
354			Carboniferous
417			Devonian
443			Silurian
490			Ordovician
543			Cambrian

- 206-144 mya
- Gymnosperms continued to be dominant
- Dinosaurs dominant land animal
  - ☐ Some attained enormous size
- First known **bird**
- Mammals present but not prevalent
- Pangaea starts to break into continents

Archaeopteryx

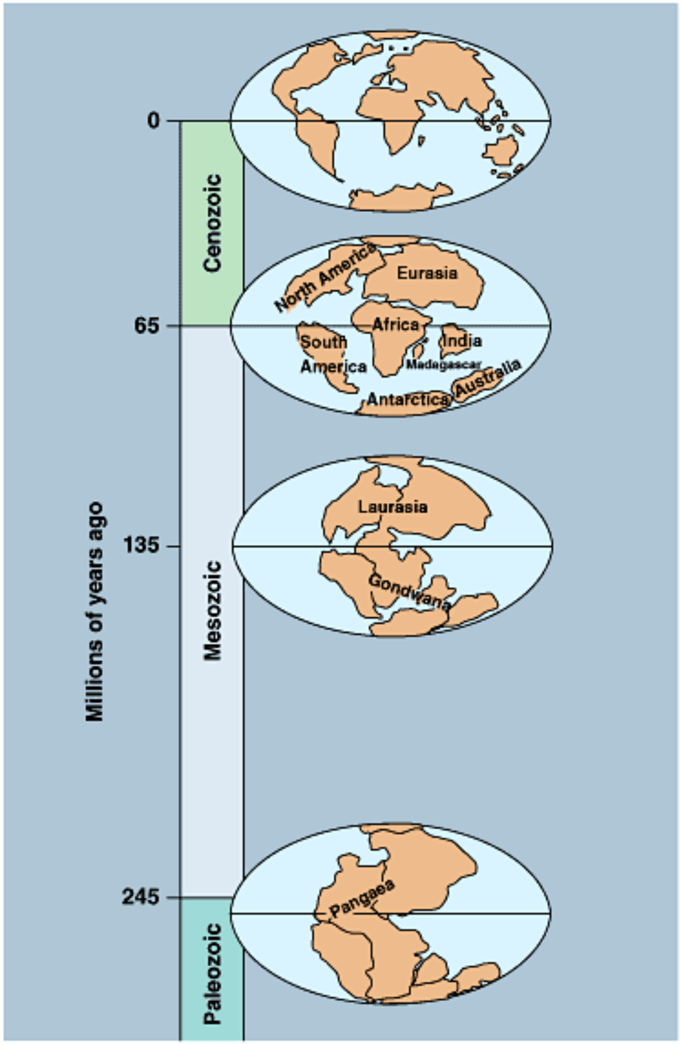


Archaeopteryx


Toothed beak
Wing claw
Airfoil wing with contour feathers
Long tail with many vertebrae

The history of continental drift

Continental drift first proposed by Alfred Wegener (1912)



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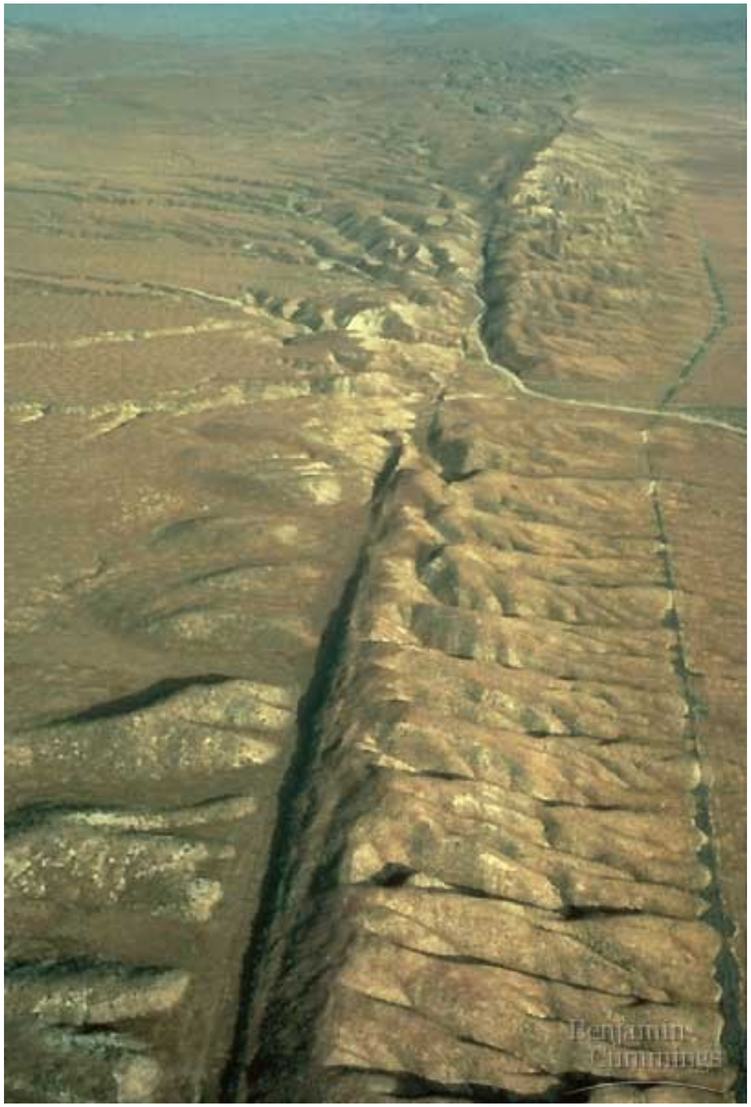
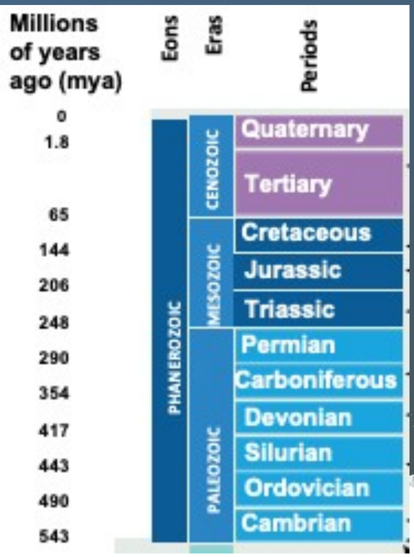
San Andreas fault



Phanerozoic Eon – Mesozoic Era – Cretaceous Period



Millions of years ago (mya)	Eons	Eras	Periods
0	PHANEROZOIC	CENOZOIC	Quaternary
1.8			Tertiary
65		MESOZOIC	Cretaceous
144			Jurassic
206			Triassic
248		PALEOZOIC	Permian
290			Carboniferous
354			Devonian
417			Silurian
443			Ordovician
490			Cambrian
543			

- 144-65 mya
- Dinosaurs still dominant on land
- Earliest flowering plants, **angiosperms**
- Another **mass extinction** at the end of the period
- Dinosaurs and many other species died out
- Large meteorite/asteroid or volcanic eruptions blamed

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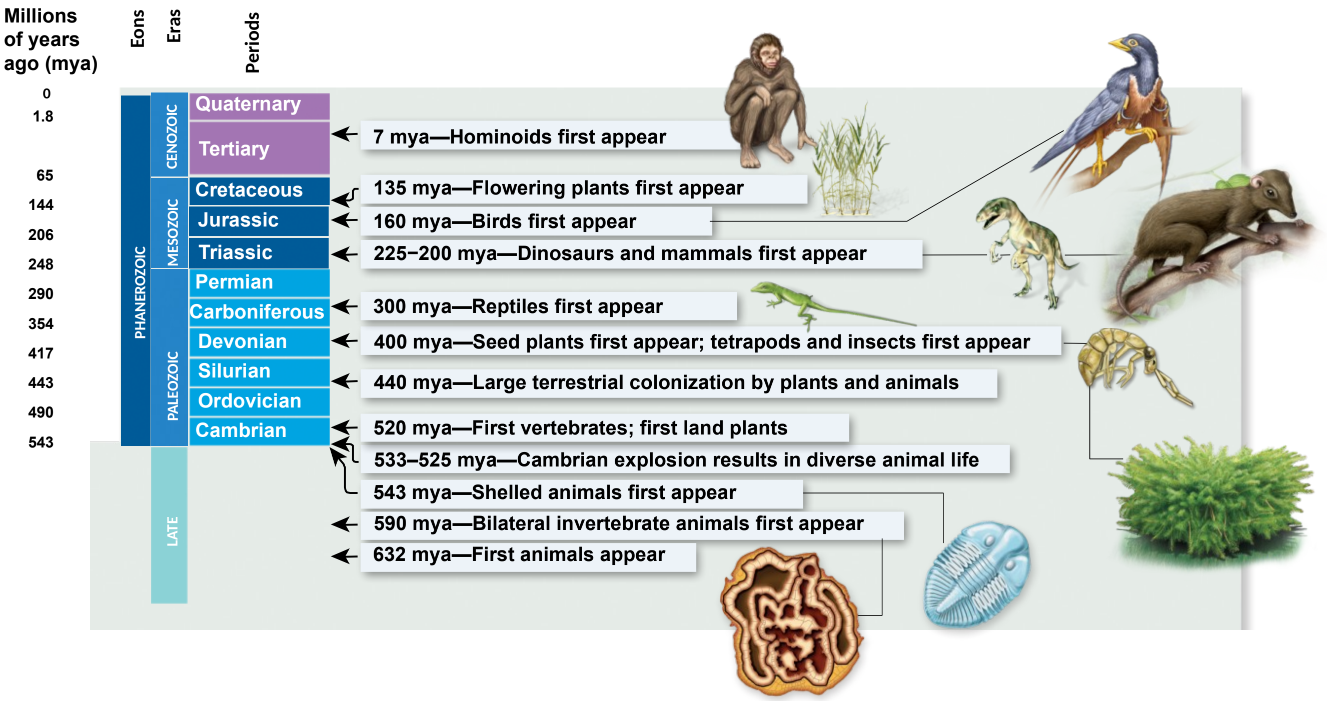


Millions of years ago (mya)

Eons

Eras

Periods

0
1.8
65
144
206
248
290
354
417
443
490
543

PHANEROZOIC

CENOZOIC
MESOZOIC
PALEOZOIC
LATE

Quaternary
Tertiary
Cretaceous
Jurassic
Triassic
Permian
Carboniferous
Devonian
Silurian
Ordovician
Cambrian

7 mya—Hominoids first appear
135 mya—Flowering plants first appear
160 mya—Birds first appear
225–200 mya—Dinosaurs and mammals first appear
300 mya—Reptiles first appear
400 mya—Seed plants first appear; tetrapods and insects first appear
440 mya—Large terrestrial colonization by plants and animals
520 mya—First vertebrates; first land plants
533–525 mya—Cambrian explosion results in diverse animal life
543 mya—Shelled animals first appear
590 mya—Bilateral invertebrate animals first appear
632 mya—First animals appear

Phanerozoic Eon – Cenozoic Era

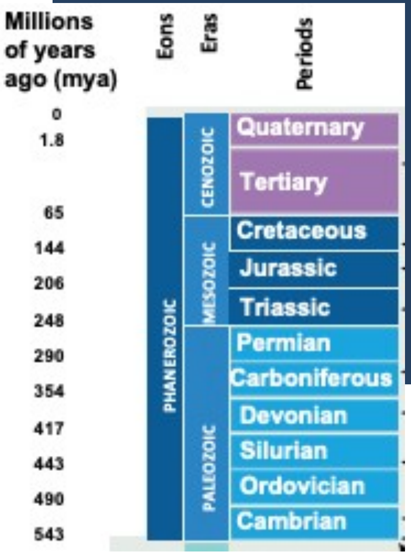
SPANS MOST RECENT 65 MILLION YEARS

TROPICAL CONDITIONS REPLACED BY A COLDER, DRIER CLIMATE

SOMETIMES CALLED **THE AGE OF MAMMALS**

AMAZING DIVERSIFICATION OF BIRDS, FISH, INSECTS, AND FLOWERING PLANTS

Phanerozoic Eon – Cenozoic Era – Tertiary Period

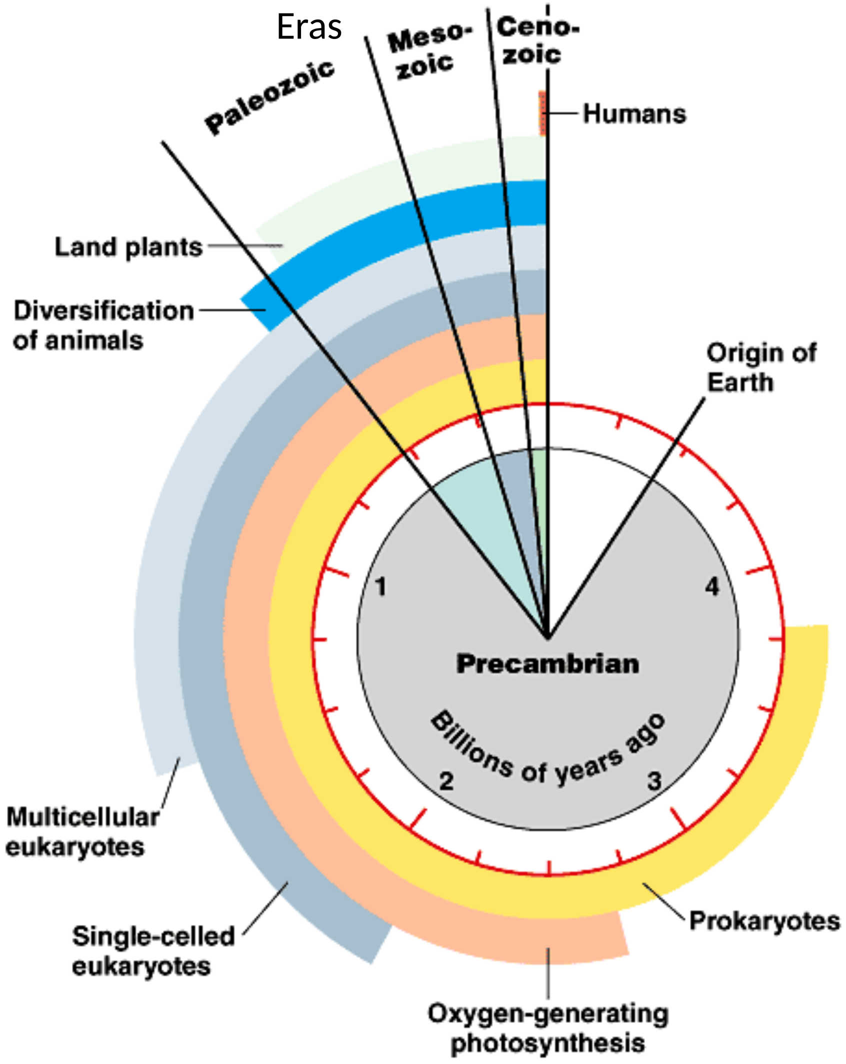


- 65-1.8 mya
- Mammals that survived expanded rapidly
- Birds and terrestrial insects diversified
- Angiosperms (flowering plants) become the dominant land plant
- Fish diversified, sharks become abundant
- Whales appeared
- **Hominids** appeared about 7 mya

Phanerozoic Eon – Cenozoic Era – Quaternary Period

- 1.8 mya to present
- Periodic ice ages covered much of Europe and North America (continuing)
- Widespread extinction of many species
- Certain hominids became more human-like
- ***Homo sapiens*** appeared 130,000 years ago

Clock analogy for some key events in evolutionary history



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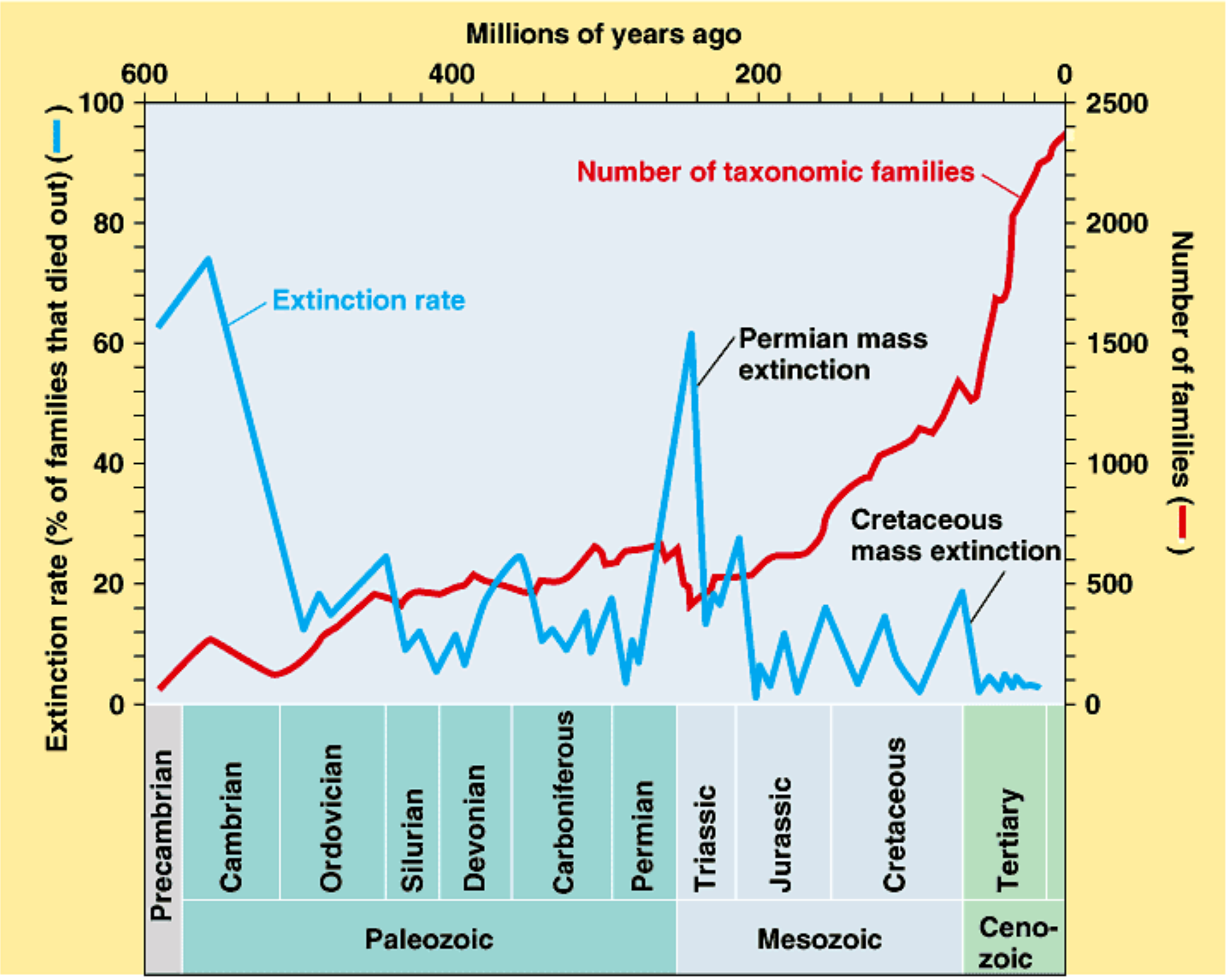
Diversity of life and periods of mass extinction



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BIOLOGY

Chapter 22 EVOLUTION AND THE ORIGIN OF SPECIES

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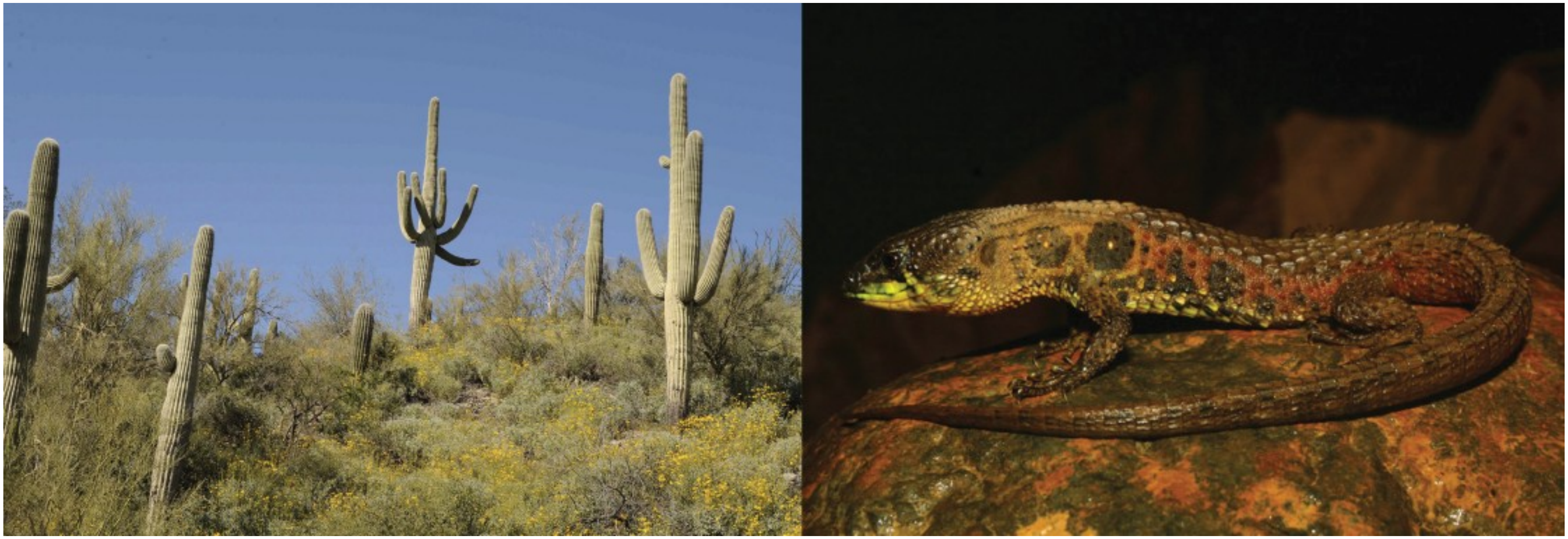
FIGURE 18.1



All organisms are products of evolution adapted to their environment. (a) Saguaro (*Carnegiea gigantea*) can soak up 750 liters of water in a single rain storm, enabling these cacti to survive the dry conditions of the Sonora desert in Mexico and the Southwestern United States. (b) The Andean semiaquatic lizard (*Potamites montanicola*) discovered in Peru in 2010 lives between 1,570 to 2,100 meters in elevation, and, unlike most lizards, is nocturnal and swims. Scientists still do no know how these cold-blood animals are able to move in the cold (10 to 15°C) temperatures of the Andean night. (credit a: modification of work by Gentry George, U.S. Fish and Wildlife Service; credit b: modification of work by Germán Chávez and Diego Vásquez, *ZooKeys*)

Basic definitions

1. Species – is difficult to define

- Group of genetically related organisms that share distinctive characteristics (traits)
- Among species that reproduce sexually, members of the same species are **capable of interbreeding** to produce viable and fertile offspring. They are reproductively isolated from other species (the Biological Species Concept)

2. Population

- Members of the same species that are likely to encounter each other and thus have the opportunity to interbreed

3. Evolution – Heritable change in one or more characteristics of a population or species from one generation to the next

a. Microevolution – changes within a population over time

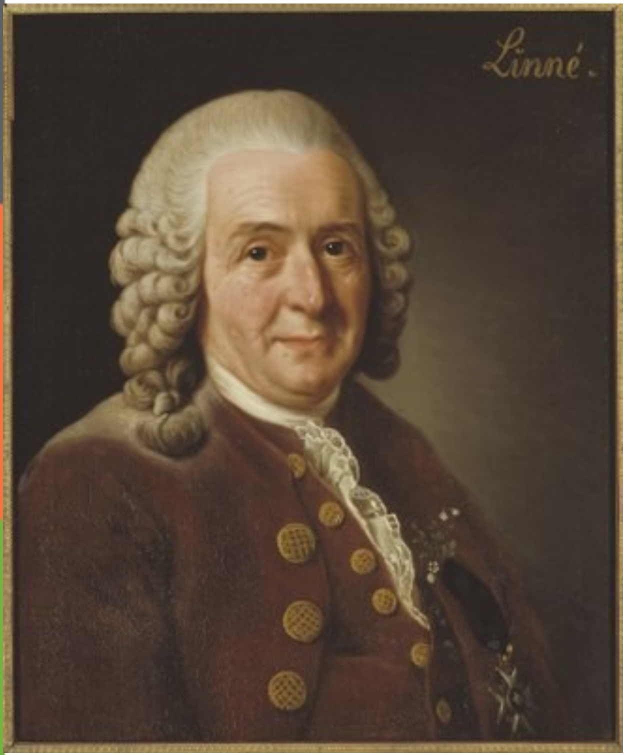
b. Macroevolution – formation of new species or species

History of Evolutionary Thought

- Plato (Greek, 428-348BC) – essence fixity (elemental forces placed by the gods)
- Aristotle (Greek, 384-322BC) – species fixity
- Key concept for both – life presents an orderly progression from “lower” organisms to “higher” forms, with humans at the top.

Mid- to late-1600s, **John Ray** was the first to carry out a thorough study of the natural world

- ☐ Developed an early classification system
- ☐ **Modern species concept –** biological definition of species



Extended by **Carolus Linnaeus** (1707-1778) **– binomial nomenclature**

However, neither proposed that evolutionary change promotes the formation of new species

Late 1700s, small number of European scientists suggest life forms are not fixed

George Buffon (1707-1788) - 1st person to discuss evolutionary type problems (comparative anatomy, earth's history is a long time-scale, inheritance from parents, struggle for existence)

Jean-Baptiste Lamarck (1744-1829) - realized that some animals remain the same while others change

- Believed living things evolved upward toward human "perfection" (From dead matter to human perfection)
- **Inheritance of acquired characteristics**
    - E.g. Giraffe necks
    - Radio Lab "Inheritance"

NEW IDEAS:

Linnaeus (1707-1778) allowed for **intraspecific variation**

Erasmus Darwin (1731-1802) (Charles' grandfather) – speculated on species evolution by Lamarckian mechanisms (knew of fossils, domesticated species, inheritance of features, mentioned "**common ancestor**")

Charles Darwin (1809-1882) – first person to articulate a **MECHANISM for evolutionary change**

INSIGHTS FROM GEOLOGY AND DEMOGRAPHY (BUILDING BLOCKS FOR DARWIN'S IDEAS)

Gradualism (James Hutton) 1795

Uniformitarianism hypothesis (Charles Lyell) 1830: Both from geology

- Slow, recurring geological processes lead to substantial change
- Earth was much older than 6,000 + years
- Book: Principles of Geology (Lyell) 1830-1833

Thomas Malthus-1766-1834: an economist (food production growth linear vs. populatio growth exponential) He said that only a fraction of any population will survive and reproduce (why?)

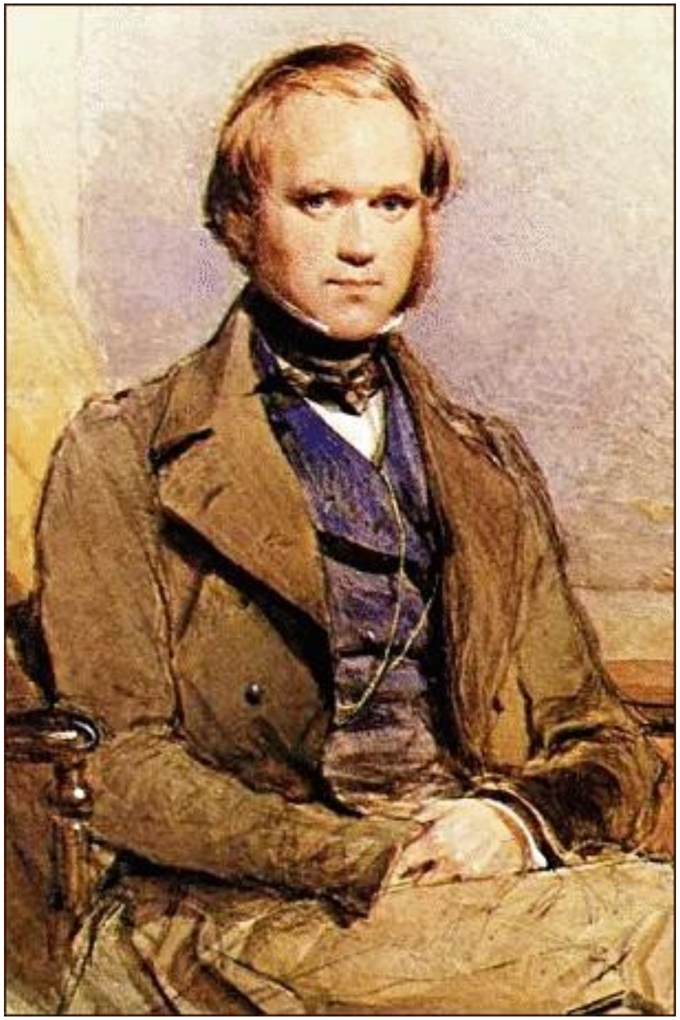
– famine, war, disease.

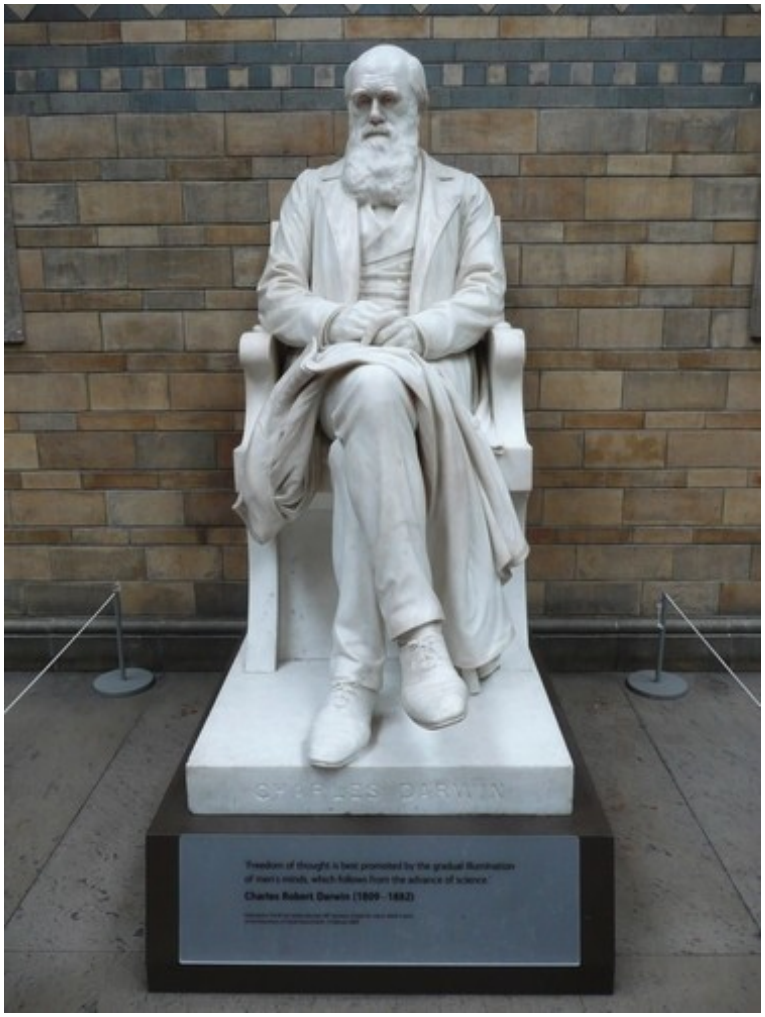
George Cuvier-1769-1832: naturalist, zoologist, paleontologist. Comparative anatomy; expanded taxonomy to Phyla; **supported extinction** as fact

Breeding of farm animals – Darwin witnessed hereditary changes caused by selective breeding

CHARLES DARWIN

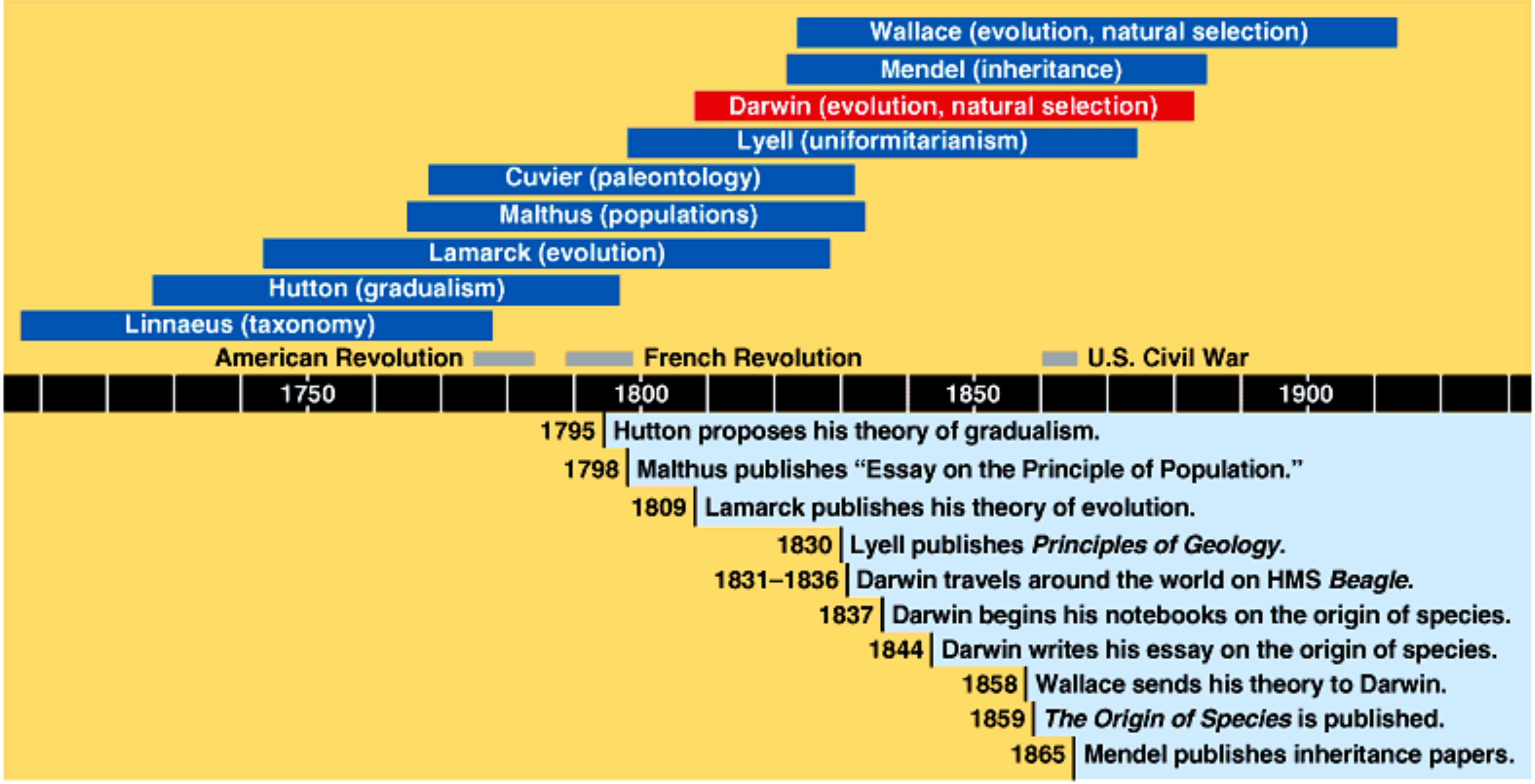
British naturalist born in 1809





CHARLES DARWIN
"Freedom of thought is best promoted by the gradual illumination of men's minds, which follows from the advance of science."
Charles Robert Darwin (1809 - 1882)

THE HISTORICAL CONTEXT OF DARWIN'S LIFE AND IDEAS



1795 | Hutton proposes his theory of gradualism.

1798 | Malthus publishes "Essay on the Principle of Population."

1809 | Lamarck publishes his theory of evolution.

1830 | Lyell publishes *Principles of Geology*.

1831–1836 | Darwin travels around the world on HMS *Beagle*.

1837 | Darwin begins his notebooks on the origin of species.

1844 | Darwin writes his essay on the origin of species.

1858 | Wallace sends his theory to Darwin.

1859 | *The Origin of Species* is published.

1865 | Mendel publishes inheritance papers.

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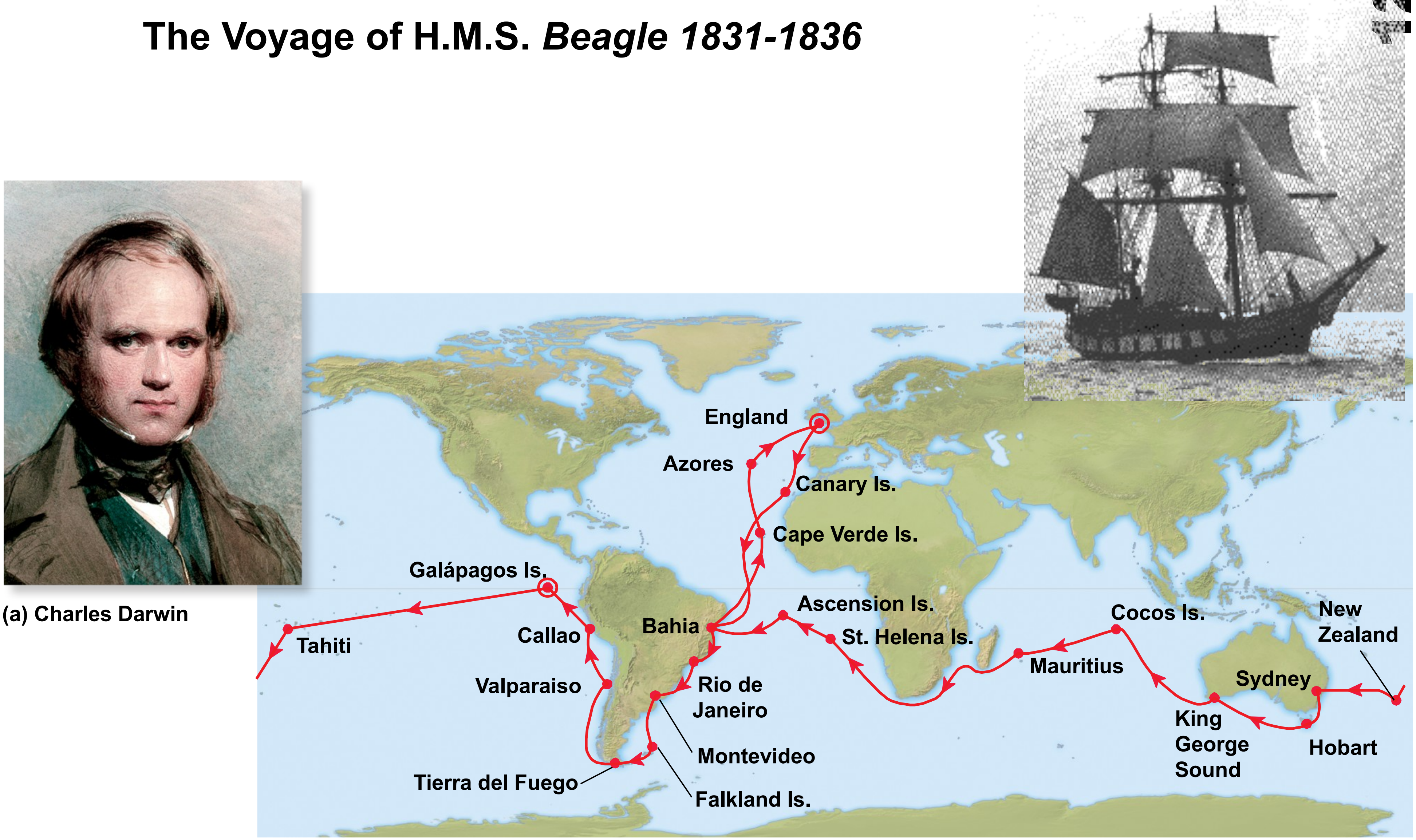
The Voyage of H.M.S. *Beagle 1831-1836*



(a) Charles Darwin

(b) The voyage of the *Beagle*

a: © PoodlesRock/Corbis

CHARLES DARWIN SUMMARY

Discovery®
CHANNEL

VOYAGE OF H.M.S. BEAGLE,1831-1836

Darwin’s ideas were most influenced by his own observations

He noticed distinctive traits of island species that allowed them to better exploit their environment. He also noted similarities between island species and those on the continent

E.g.**Galápagos Islands finches (arrived a few million years ago)**

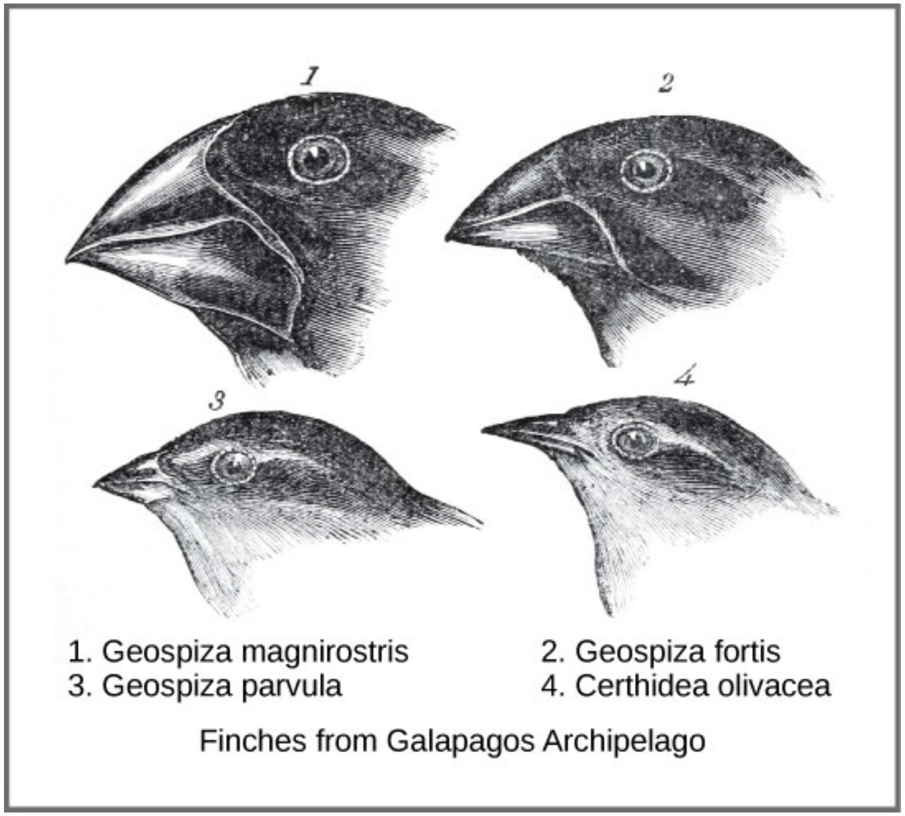
- Saw similarities in species yet noted differences that provided them with specialized feeding strategies – **ADAPTIVE RADIATION**

20 years of subsequent thought

Publication precipitated by Wallace

GALÁPAGOS FINCHES

FIGURE 18.2



Darwin observed that beak shape varies among finch species. He postulated that the beak of an ancestral species had adapted over time to equip the finches to acquire different food sources.

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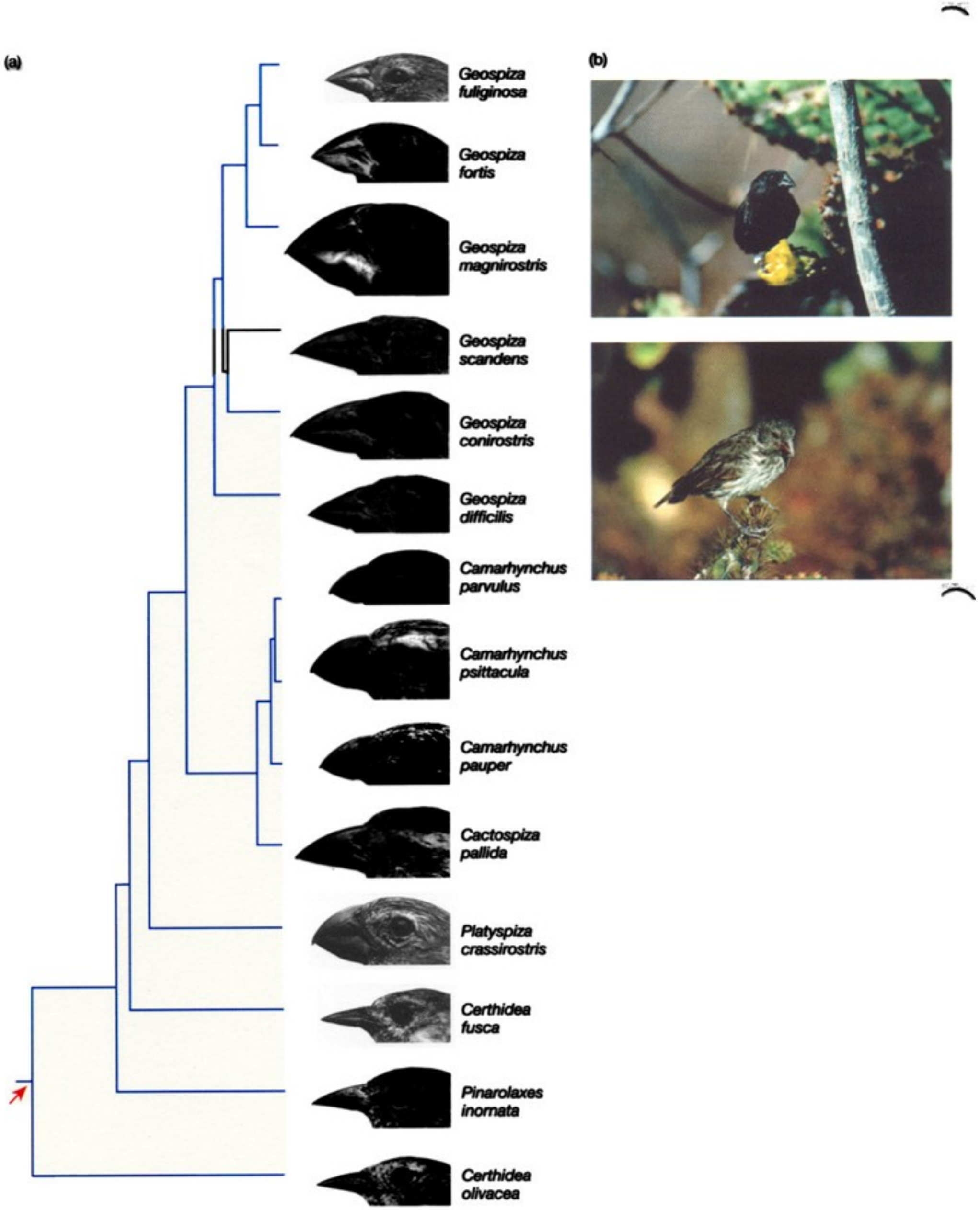
Table 23.1 A Comparison of Beak Type and Diet Among the Galápagos Finches That Darwin Studied

Type of finch/diet	Species		Type of beak
Ground finches			
Ground finches have beaks shaped to crush various sizes of seeds; large beaks can crush large seeds, whereas smaller beaks are better for crushing small seeds.	Large ground finch (*Geospiza magnirostris*)		Crushing
	Medium ground finch (*G. fortis*)		
	Small ground finch (*G. fuliginosa*)		
	Sharp-billed ground finch (*G. difficilis*)		
Vegetarian finch			
Vegetarian finches have crushing beaks to pull buds from branches.	Vegetarian finch (*Platyspiza crassirostris*)		Crushing
Tree finches			
Tree finches have grasping beaks to pick insects from trees. Those with heavier beaks can also break apart wood in search of insects.	Large tree finch (*Camarhynchus psittacula*)		Grasping
	Medium tree finch (*Camarhynchus pauper*)		
	Small tree finch (*Camarhynchus parvulus*)		
Tree and warbler finches			
These finches have probing beaks to search for insects in crevices and then to pick them up. The woodpecker finch can also use a cactus spine for probing.	Mangrove finch (*Cactospiza heliobates*)		Probing
	Woodpecker finch (*Camarhynchus pallidus*)		
	Warbler finch (*Certhidea olivacea*)		
Cactus finches			
Cactus finches have probing beaks to open cactus fruits and take out seeds.	Large cactus finch (*G. conirostris*)		Probing
	Cactus finch (*G. scandens*)		

T-13 Fig. 3.1 The Galápagos finches, and the medium ground finch Geospiza fortis



Evolutionary Analysis, 2nd Edition
Scott Freeman and Jon C. Herron

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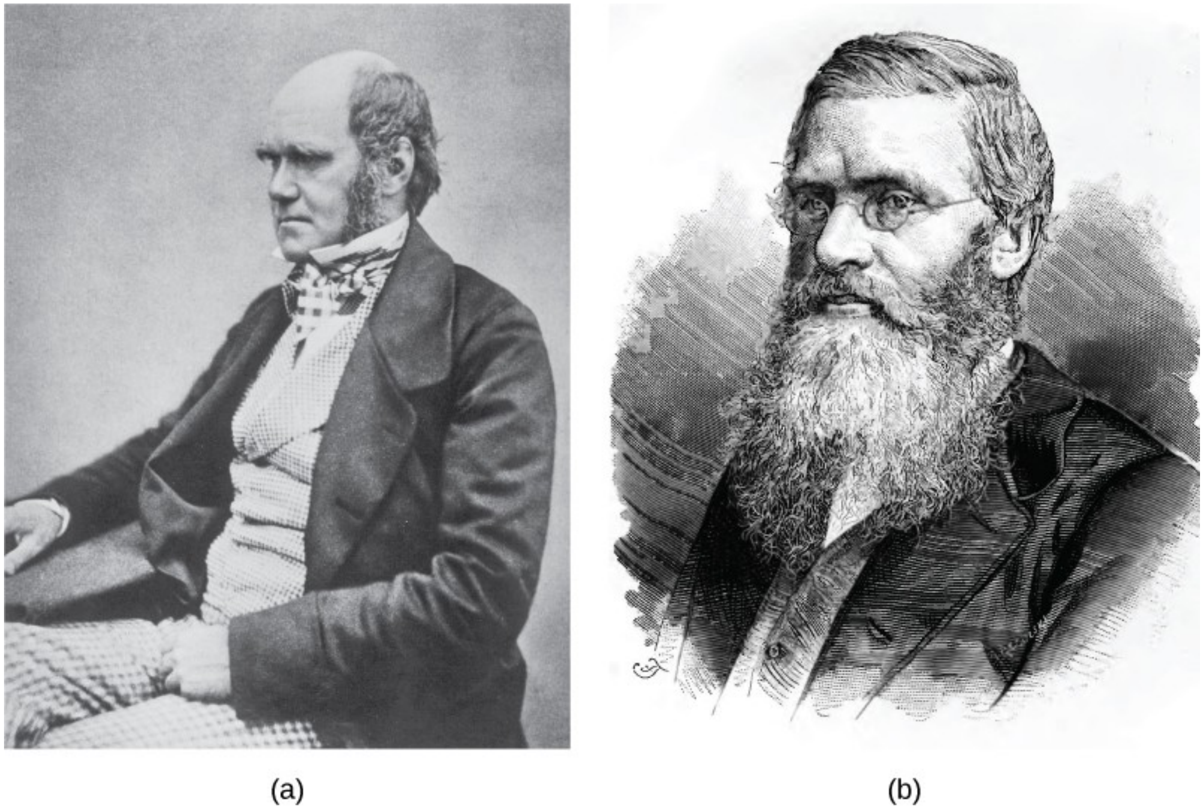
Pearson Education
Upper Saddle River, NJ 07458

On the Origin of Species: By Charles Darwin, 1859

“The most striking and important fact for us in regard to the inhabitants of islands, is their affinity to those of the nearest mainland, without being actually the same species. [In] the Galapagos Archipelago ... almost every product of the land and water bears the unmistakable stamp of the American continent. There are twenty-six land birds, and twenty-five of these are ranked by Mr. Gould as distinct species, supposed to have been created here; yet the close affinity of most of these birds to American species in every character, in their habits, gestures, and tones of voice, was manifest. ... The naturalist, looking at the inhabitants of these volcanic islands in the Pacific, distant several hundred miles from the continent, yet feels that he is standing on American land. Why should this be so? Why should the species which are supposed to have been created in the Galapagos Archipelago, and nowhere else, bear so plain a stamp of affinity to those created in America? There is nothing in the conditions of life, in the geological nature of the islands, in their height or climate, or in the proportions in which the several classes are associated together, which resembles closely the conditions of the South American coast: In fact there is a considerable dissimilarity in all these respects. On the other hand, there is a considerable degree of resemblance in the volcanic nature of the soil, in climate, height, and size of the islands, between the Galapagos and Cape de Verde Archipelagos: But what an entire and absolute difference in their inhabitants! The inhabitants of the Cape de Verde Islands are related to those of Africa, like those of the Galapagos to America. I believe this grand fact can receive no sort of explanation on the ordinary view of independent creation; whereas on the view here maintained, it is obvious that the Galapagos Islands would be likely to receive colonists, whether by occasional means of transport or by formerly continuous land, from America; and the Cape de Verde Islands from Africa; and that such colonists would be liable to modification — the principle of inheritance still betraying their original birthplace.”

FIGURE 18.3


(a) (b)

Both (a) Charles Darwin and (b) Alfred Wallace wrote scientific papers on natural selection that were presented together before the Linnean Society in 1858.

HHMI video about Darwin and Wallace

TWO major components of Darwin’s thinking:

1. Existing species have evolved from previous ancestral species (which are usually extinct)

2. The mechanism for this is Natural Selection

Darwin formulated Theory of Evolution by Natural Selection by mid-1840s – DESCENT WITH MODIFICATION THROUGH VARIATION AND NATURAL SELECTION

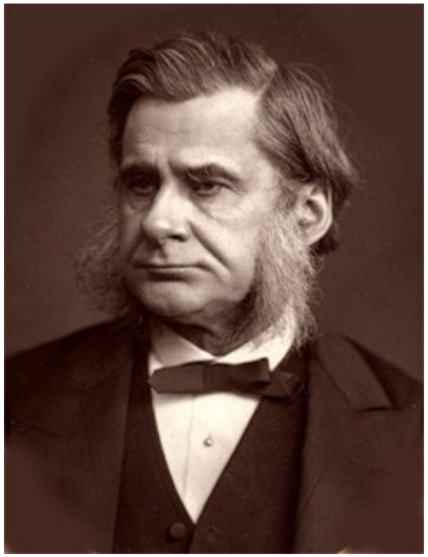
Spent several additional years studying barnacles (and discussing his ideas, with **Thomas Huxley-"Darwin's Bulldog"** – a biologist and comparative anatomist)

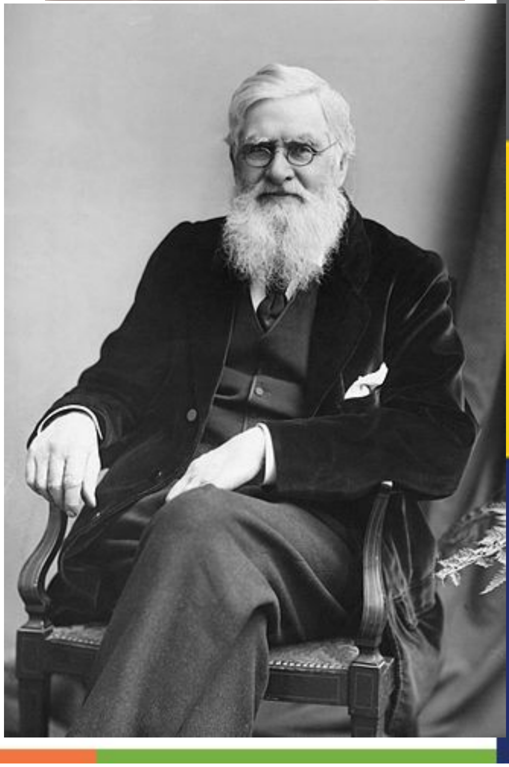
1856, began writing "the Origin"

1858, **Alfred Wallace** sent Darwin an unpublished manuscript proposing many of the same ideas

Darwin's and Wallace's papers were published and presented together at Linnean Society

1859, Darwin's ***On the Origin of Species* …** was published





THE THEORY OF NATURAL SELECTION: DARWIN'S FOUR POSTULATES

1 Individuals within species are variable

2 Some of these variations are passed on to offspring

3 More offspring are produced than can survive (because of resource limitations)

4 Survival and subsequent reproduction are NOT random. Those individuals who survive and reproduce do so because of favorable traits – they are NATURALLY SELECTED

DARWIN'S POSTULATES ARE TESTABLE: AND THEY HAVE BEEN TESTED ON THE SPECIES OF FINCHES HE ORIGINALLY OBSERVED

Are populations variable?

Is some of that variation heritable?

Is there an excess of offspring, with differential reproduction?

Are survival and reproduction non-random?

PETER AND ROSEMARY GRANT OBSERVED CONTEMPORARY NATURAL SELECTION IN GALÁPAGOS FINCHES

Grants focused much of their work on Daphne Major – moderately isolated, undisturbed habitat and resident finches

Compared beak sizes of parents and offspring over many years

Birds with larger beaks survived better during drought years

In the year after drought, average beak depth increases

RADIO LAB

Inheritance

Leaving Your Lamarck (28:06-5:30)

You Are What Your Grandpa Eats

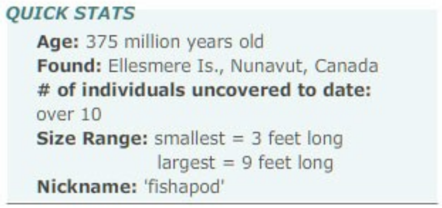
What If There Was No Destiny?

Evidence of Evolutionary Change 22

- Fossil record
- Biogeography
- Convergent evolution
- Selective breeding
- Homologies
  - Anatomical
  - Developmental
  - Molecular

FOSSILS: FISHAPOD (*TIKTAALIK ROSEAE*)

- Illuminates steps leading to **evolution of tetrapods**
- **Transitional form** – provides link between earlier and later forms
- Had broad skull, flexible neck, eyes on top of head, primitive wrist and five fingers
- Could peek above water and look for prey



QUICK STATS

Age: 375 million years old
Found: Ellesmere Is., Nunavut, Canada
# of individuals uncovered to date: over 10
Size Range: smallest = 3 feet long
largest = 9 feet long
Nickname: 'fishapod'

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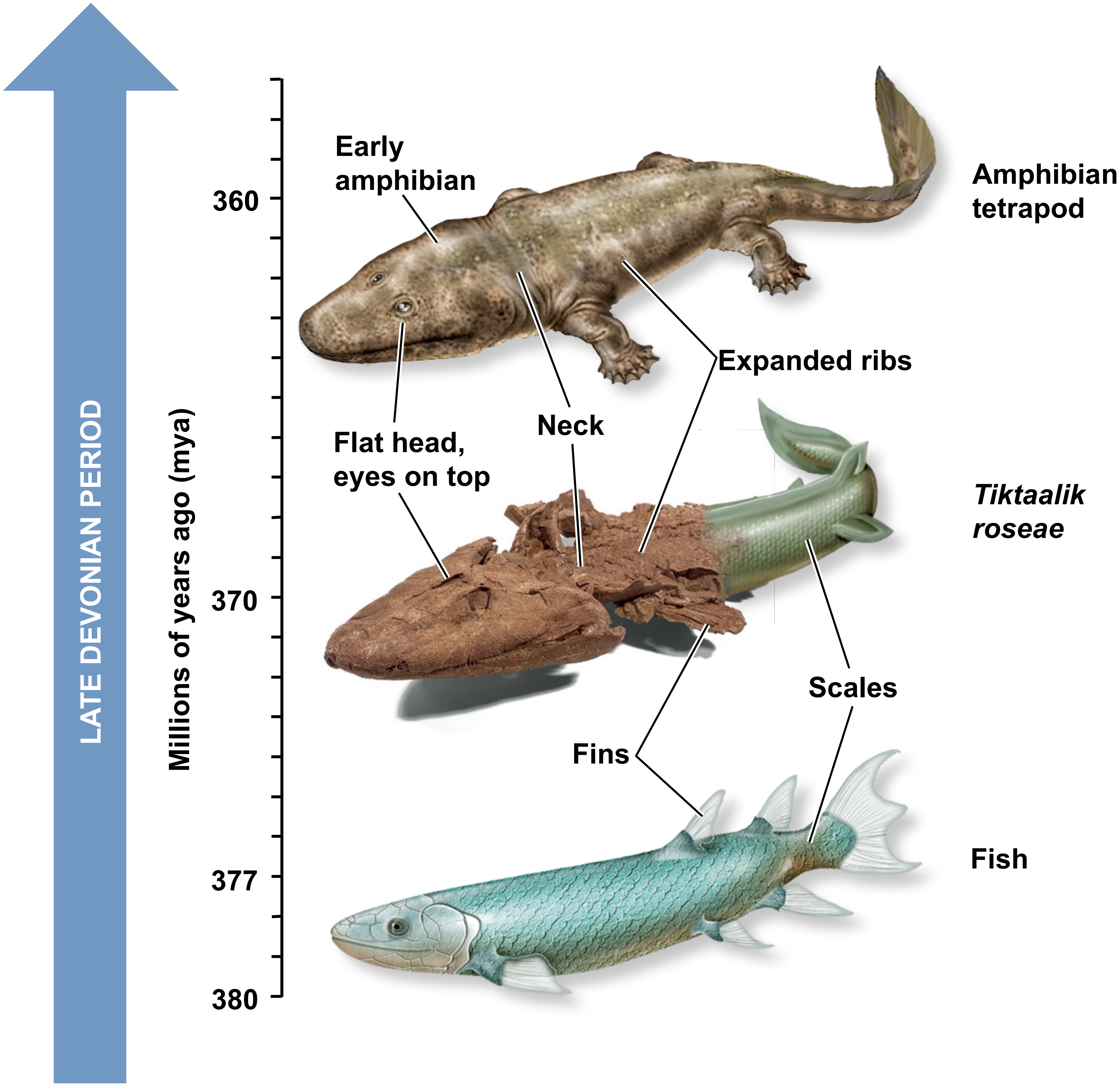
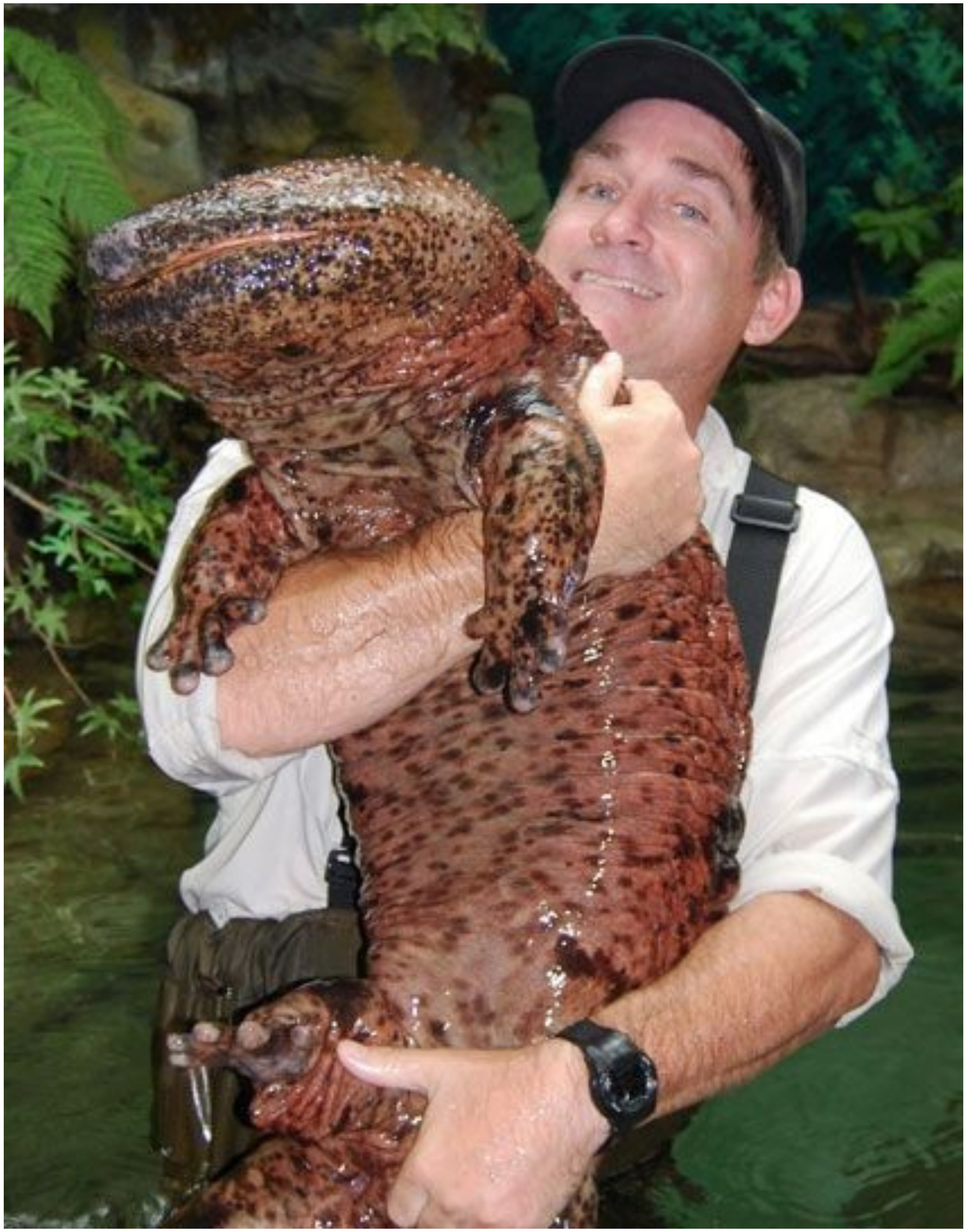


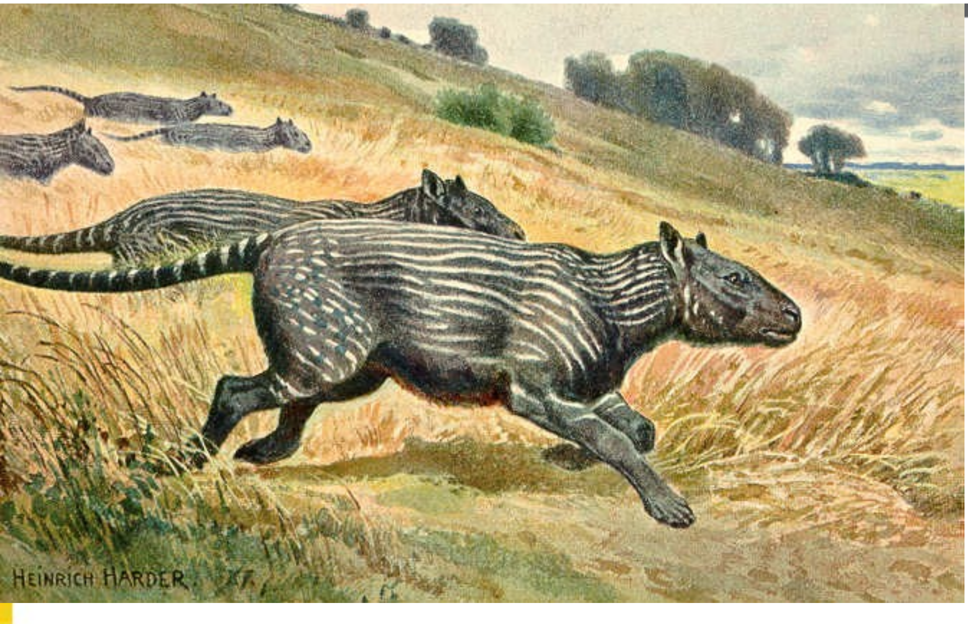
(middle): © T. Daeschler/VIREO

GIANT SALAMANDER

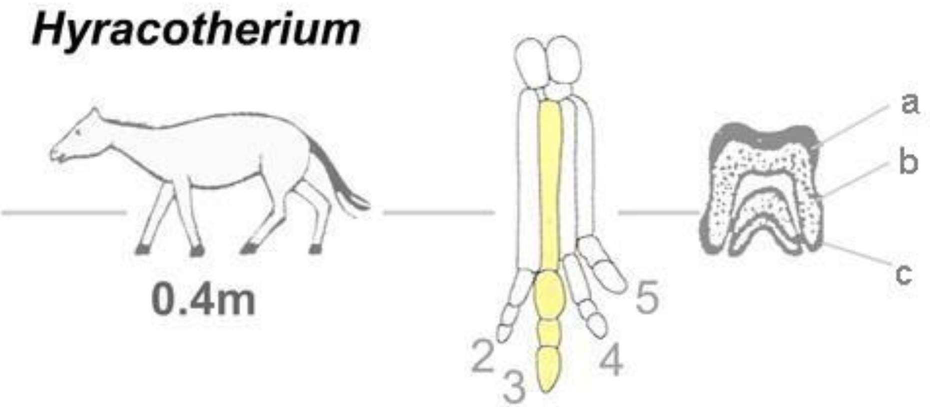


FOSSILS: HORSES

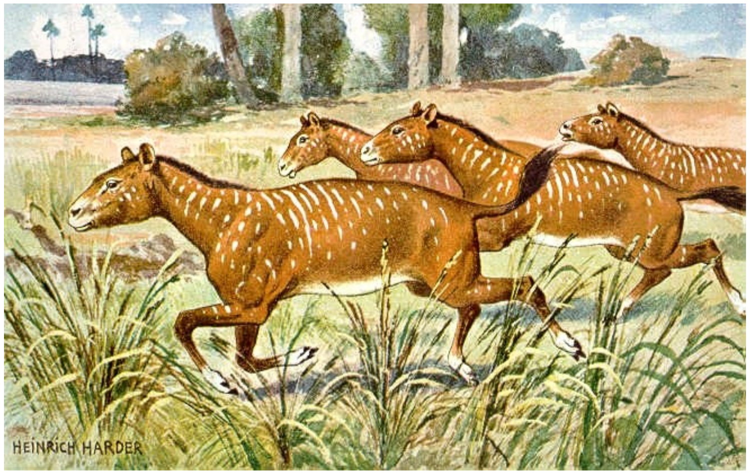
- Interesting case of how evolution involves **adaptation to changing environments**
- Fossil record has revealed adaptive changes in size, foot anatomy, and tooth morphology
- Changes can be attributed to natural selection producing adaptations to changing global climates
  - Large dense forests (in forest - dog-sized, ate tender leaves, multiple toes, soft foot), replaced with grassland
  - Run faster, eat tougher food (taller, ate tough grasses, 1 toe, hoof)



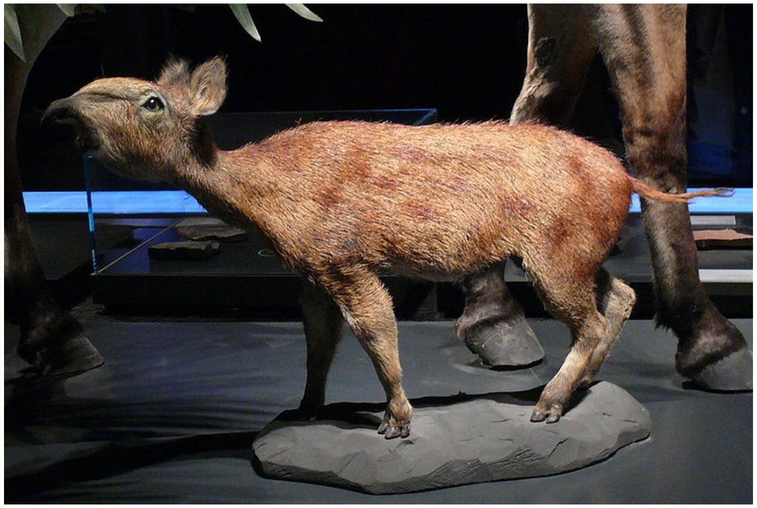
Phenacodus: Ancestor to modern Perissodactyla (odd-toed ungulates) 55mya



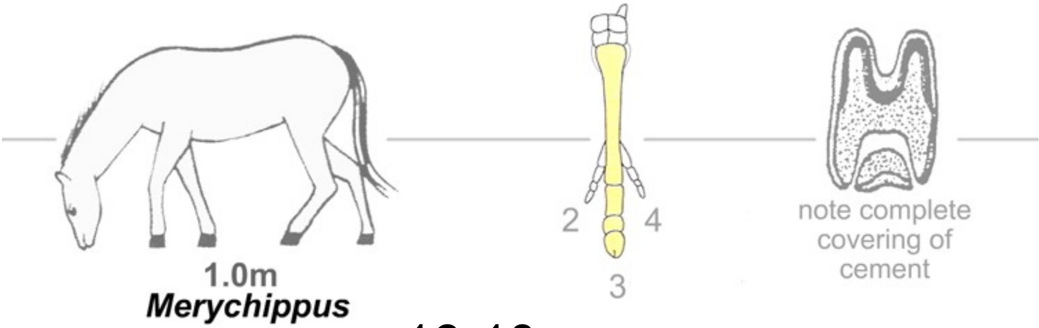
Eohippus 52mya with left forefoot (third metacarpal colored) and tooth (a enamel ; b dentin; c cement)



Mesohippus 32-24mya

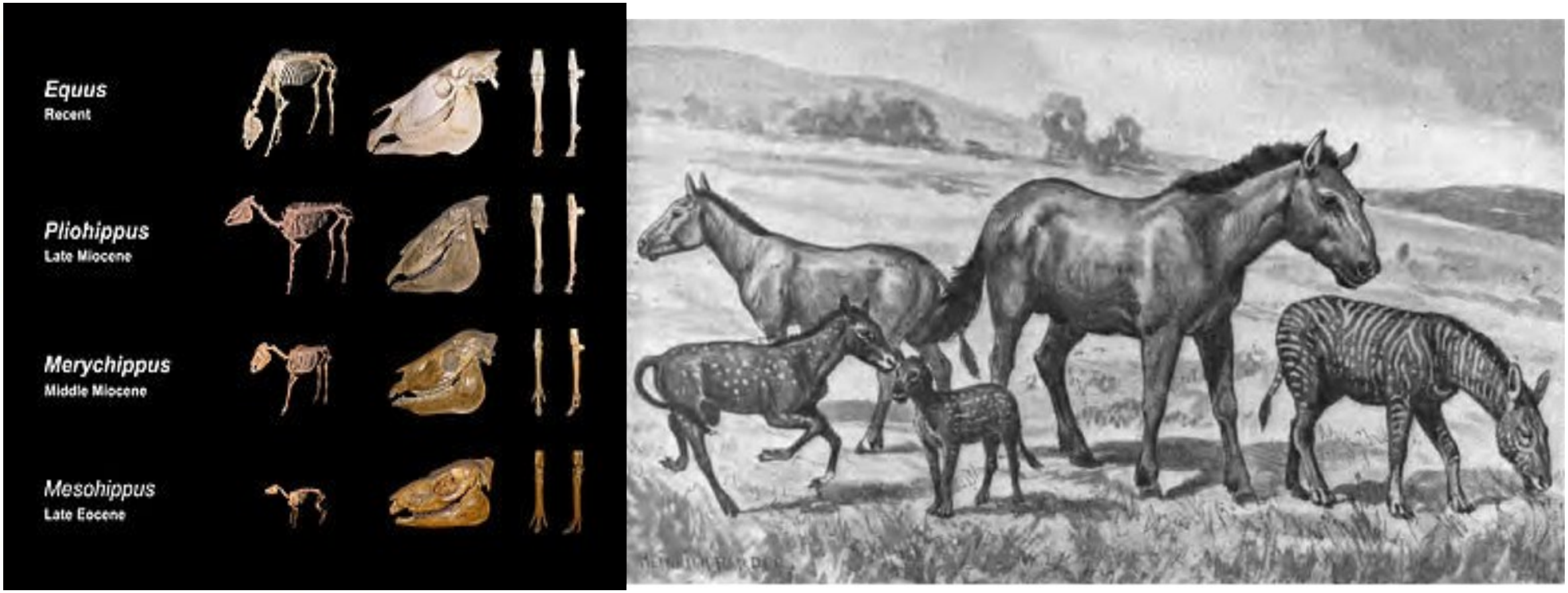


Eurohippus 47mya



16-10mya

FIGURE 18.6



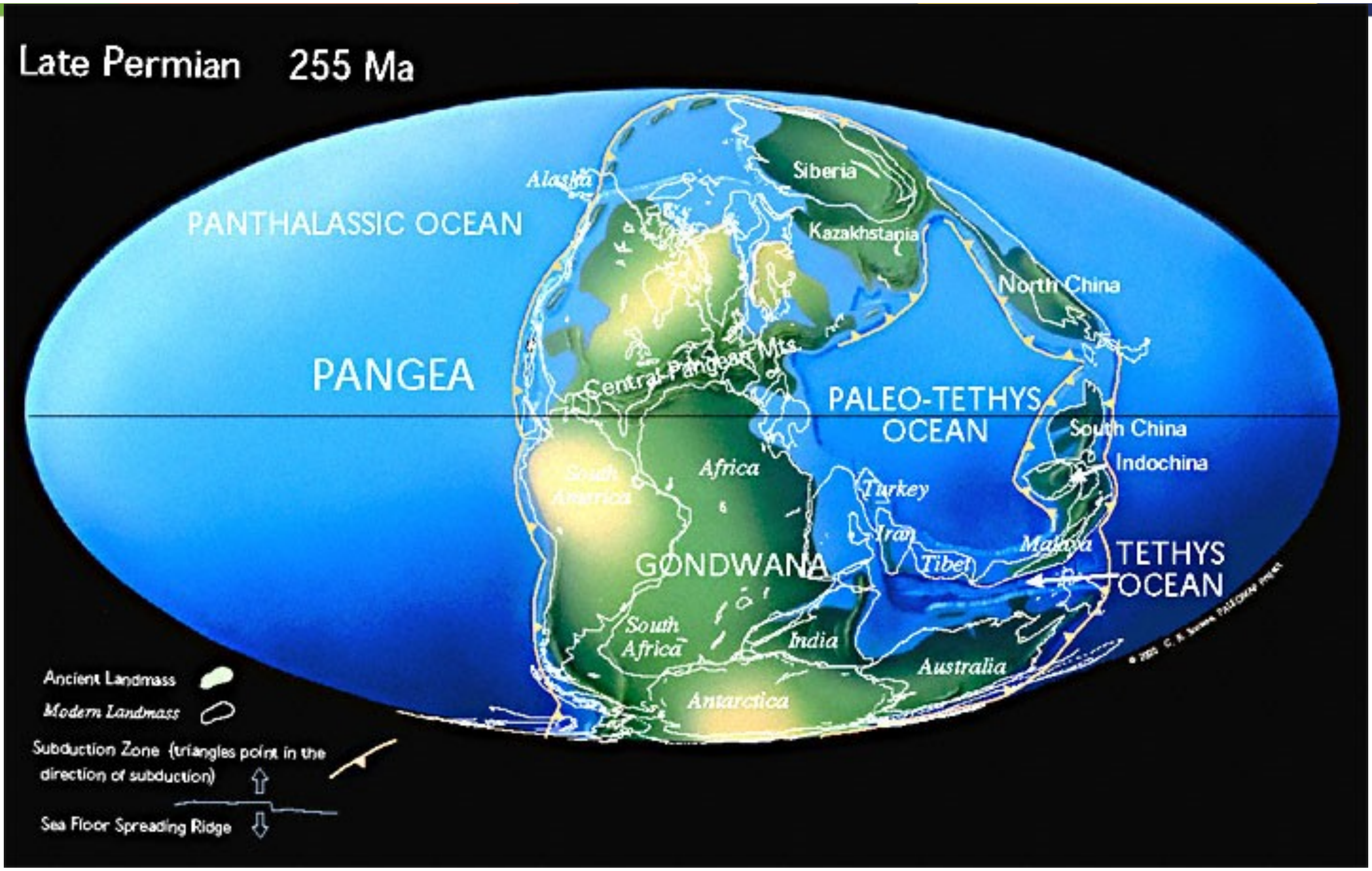
(a) (b)

In this (a) display, horse evolution from *Mesohippus (32-24*mya*)* to *Equus* (4-4.5mya). An artist’s rendition of (b) extinct species of the genus *Equus* reveals that these ancient species resembled the modern horse (*Equus ferus*) but varied in size.

BIOGEOGRAPHY

Study of the geographical distribution of extinct and modern species.

Species present prior to the break up of Pangaea are often found worldwide. Species that evolved after the break up may be found in specific areas of the planet.



Evolution of major animal groups correlated with known changes in the distribution of land masses on the Earth

First mammals (egg laying and marsupials) arose 225 mya when Australia was still connected

Placental mammals arose 80 mya after Australia separated

Australia has no large, terrestrial placental mammals (until humans arrived on the continent)

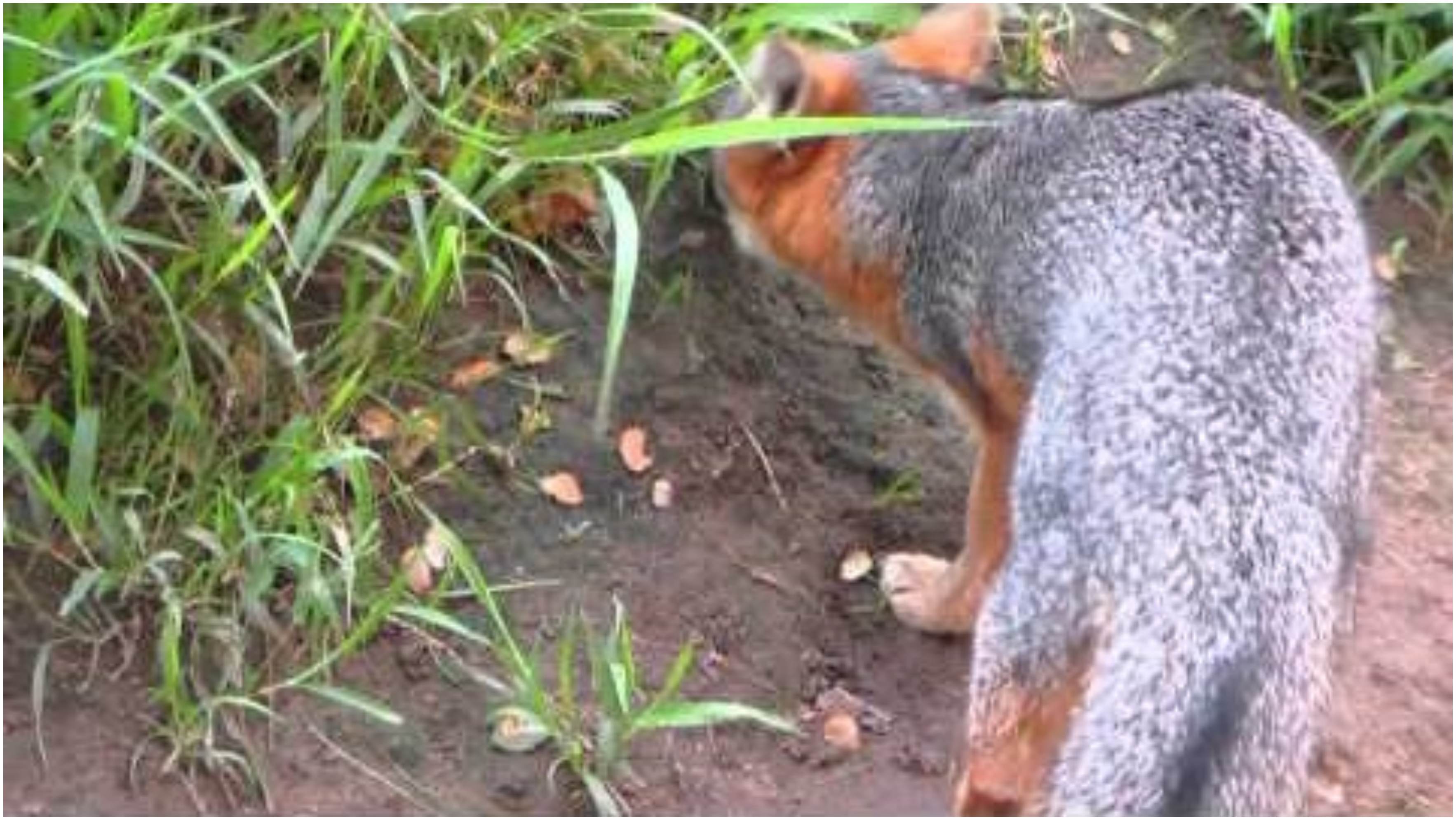
CHANNEL ISLAND FOX

Isolated continents and island groups have evolved their own distinct plant and animal communities

- **Endemic** – naturally found only in a particular location

E.g.: **Island fox** (*Urocyon littoralis*) evolved from mainland gray fox (*Urocyon cinereoargenteus*)

CHANNEL ISLAND FOX



The Santa Barbara Independent

Channel Island Foxes Back in Action

Recovery Effort Deemed Wild Success

Thursday, May 23, 2013

By Jack Crosbie

If you've been out to the Channel Islands recently, chances are you've seen the foxes — they're small, curious, and undeniably cute. Fifteen years ago, however, seeing one in the wild would have been extremely rare. Over-predation by golden eagles — attracted to the islands by the abundance of nonnative sheep and feral pigs — had nearly wiped out the bite-sized canids, driving the three subspecies' combined population down to less than 100 individuals by 1999.

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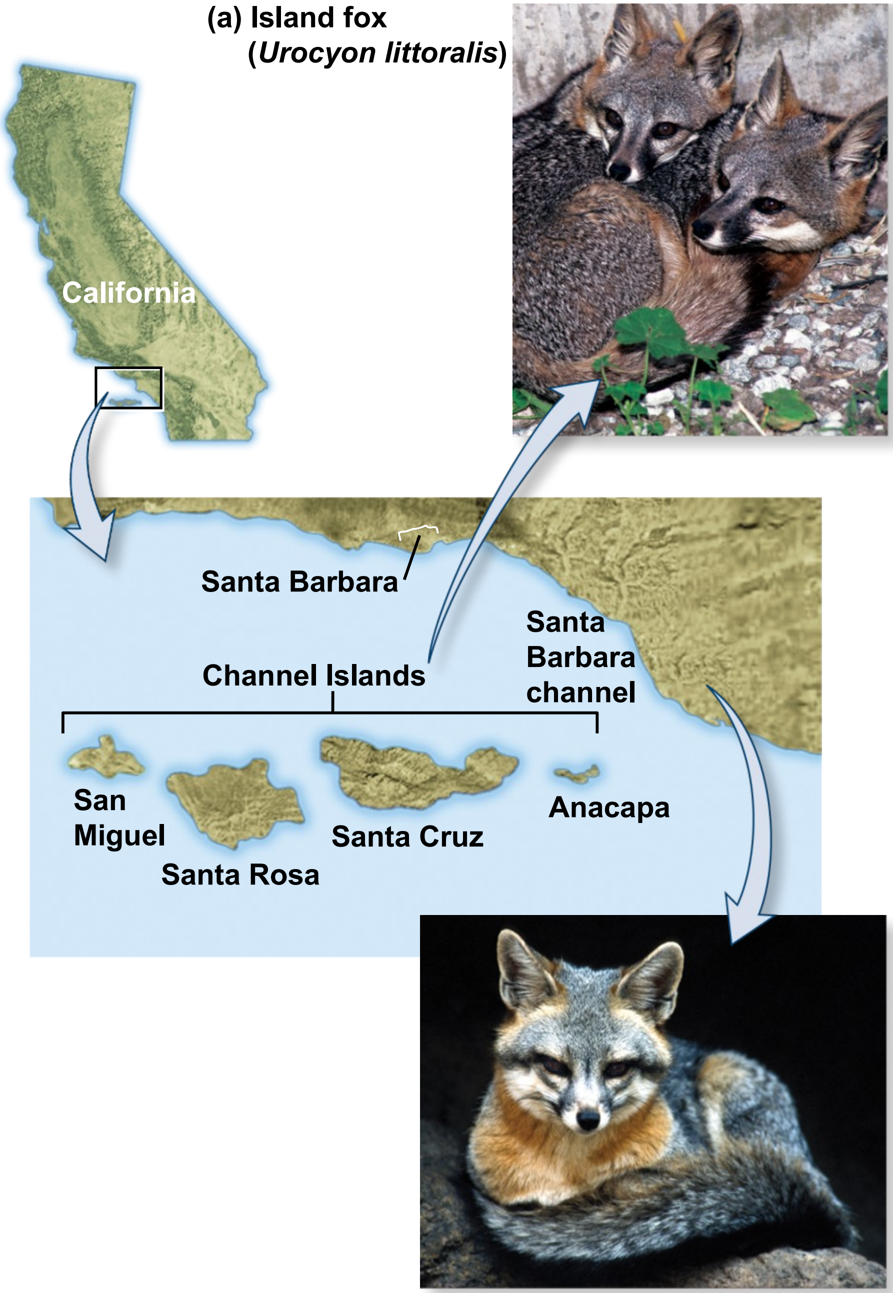
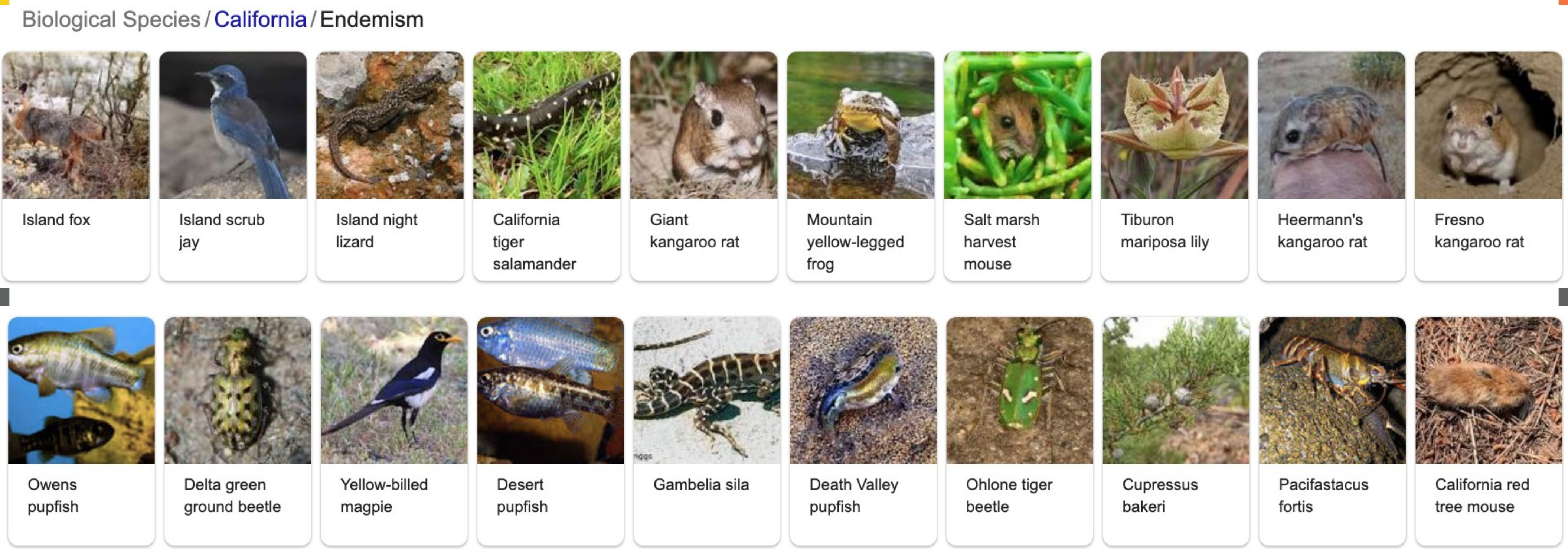


(a) Island fox (*Urocyon littoralis*)

(b) Gray fox (*Urocyon cinereoargenteus*)

a: © Wm. Grenfell/Visuals Unlimited; b: © Prisma Bildagentur AG/Alamy

CALIFORNIA ENDEMIC SPECIES



Biological Species / California / Endemism

Island fox

Island scrub jay

Island night lizard

California tiger salamander

Giant kangaroo rat

Mountain yellow-legged frog

Salt marsh harvest mouse

Tiburon mariposa lily

Heermann's kangaroo rat

Fresno kangaroo rat

Owens pupfish

Delta green ground beetle

Yellow-billed magpie

Desert pupfish

Gambelia sila

Death Valley pupfish

Ohlone tiger beetle

Cupressus bakeri

Pacifastacus fortis

California red tree mouse

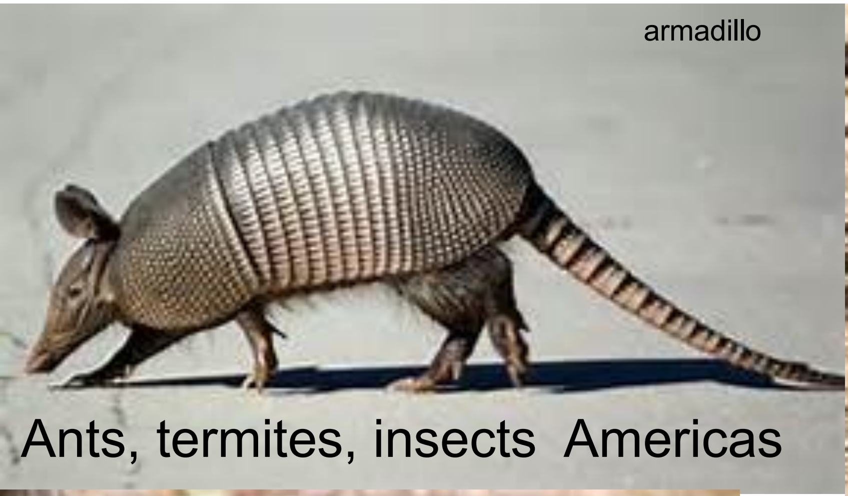
KANGAROO RAT

CONVERGENT EVOLUTION

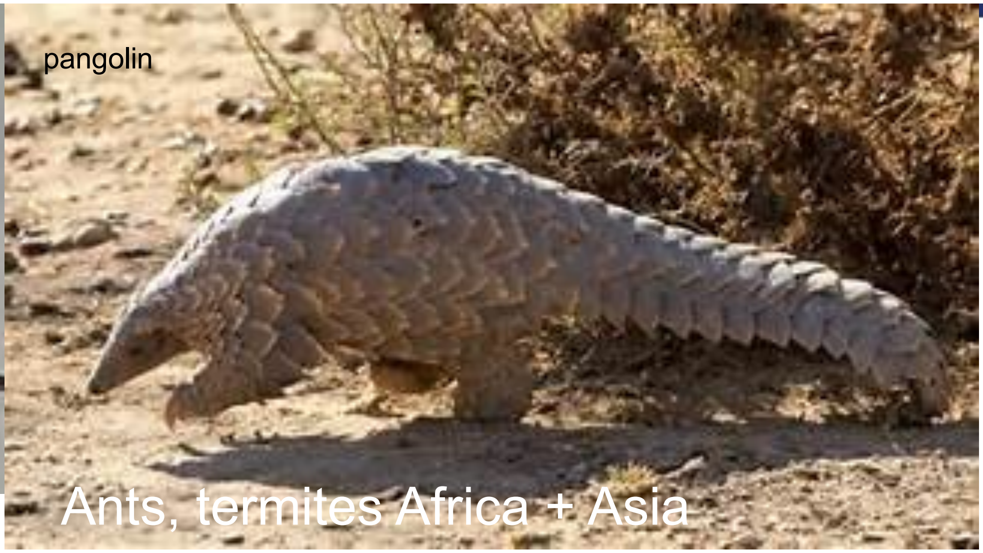
Two different species from different lineages show similar characteristics because they occupy similar environments

Examples:

- **Giant anteater** and **echidna** both have long snouts and tongues to feed on ants
- **Aerial rootlets** for clinging: in English ivy and wintercreeper
- **Antifreeze proteins** in different, very cold water fish
- **Analogous** structures

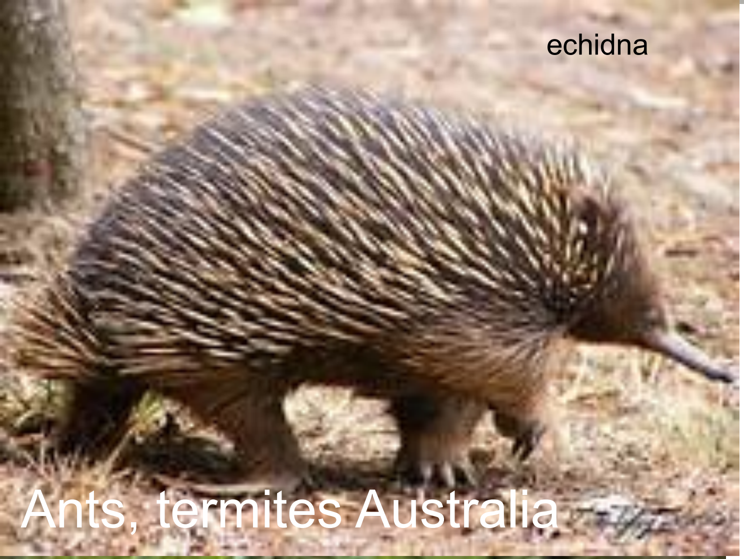

armadillo

Ants, termites, insects Americas

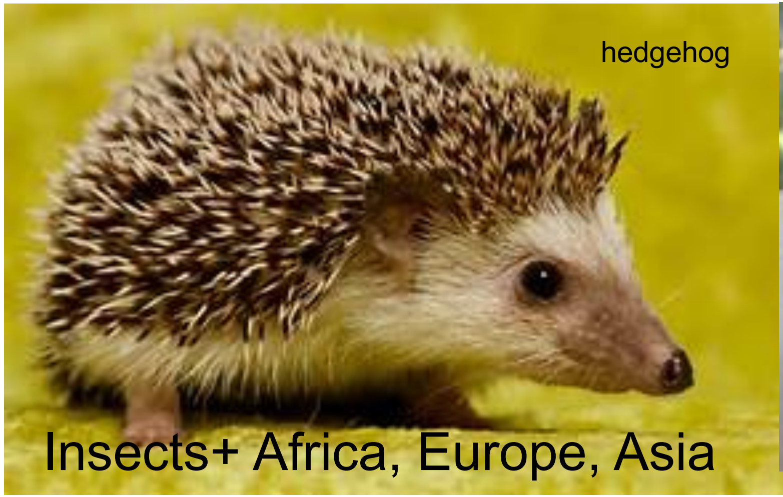

pangolin

Ants, termites Africa + Asia

[Pangolin YouTube]

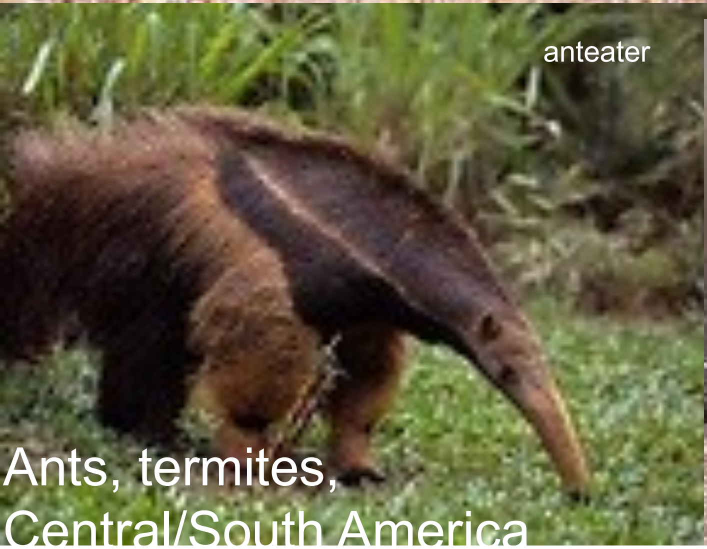

echidna

Ants, termites Australia

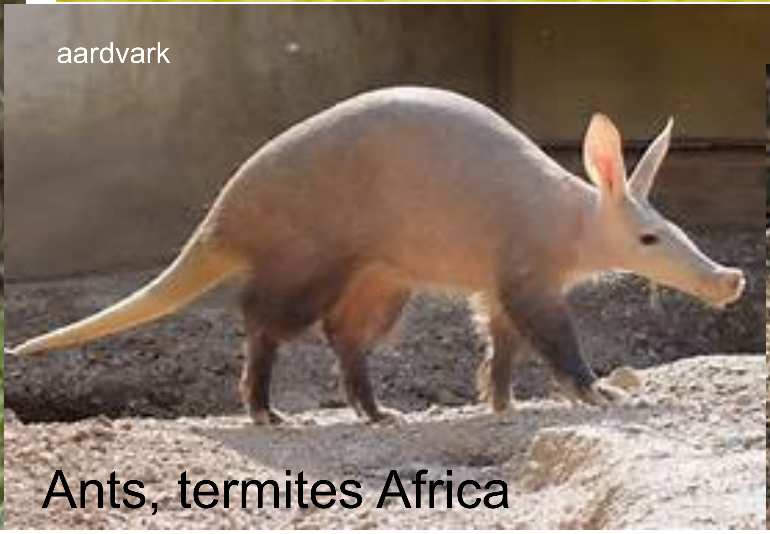

hedgehog

Insects+ Africa, Europe, Asia

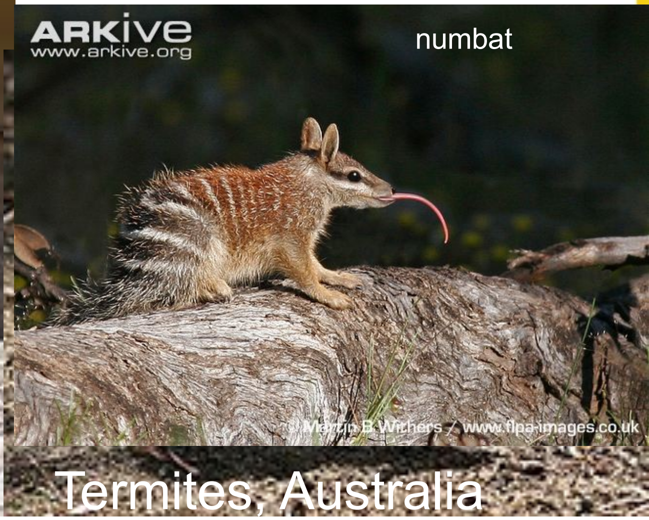
“Hoglet”


anteater

Ants, termites, Central/South America


aardvark

Ants, termites Africa

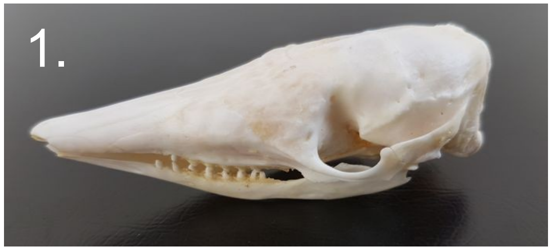


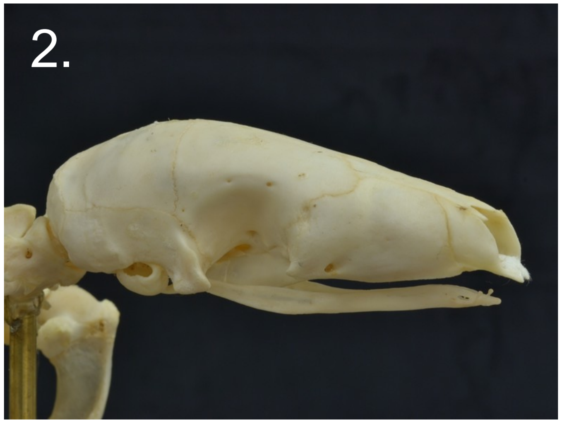
numbat

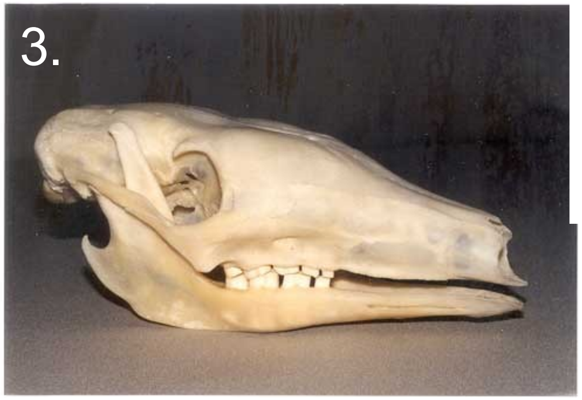
Termites, Australia

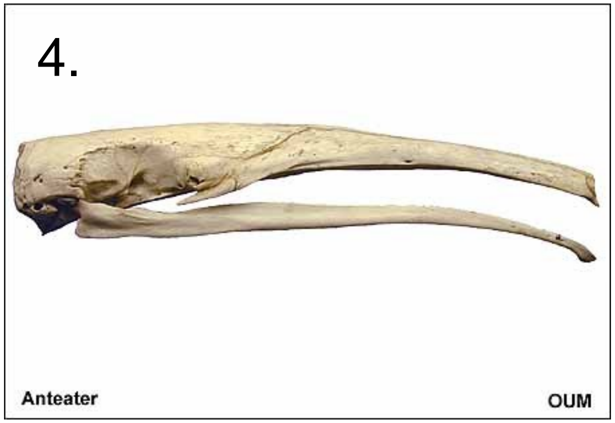
CONVERGENT EVOLUTION IN SKULLS

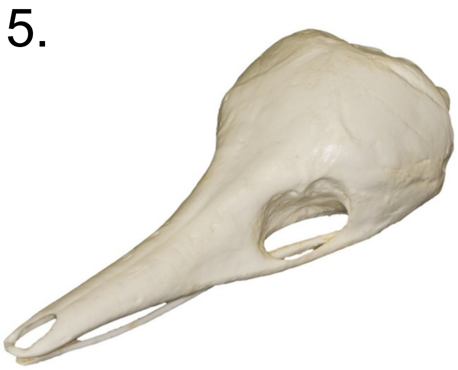
1. Seven-banded armadillo
2. Pangolin
3. Aardvark
4. Anteater
5. Short-nosed echidna





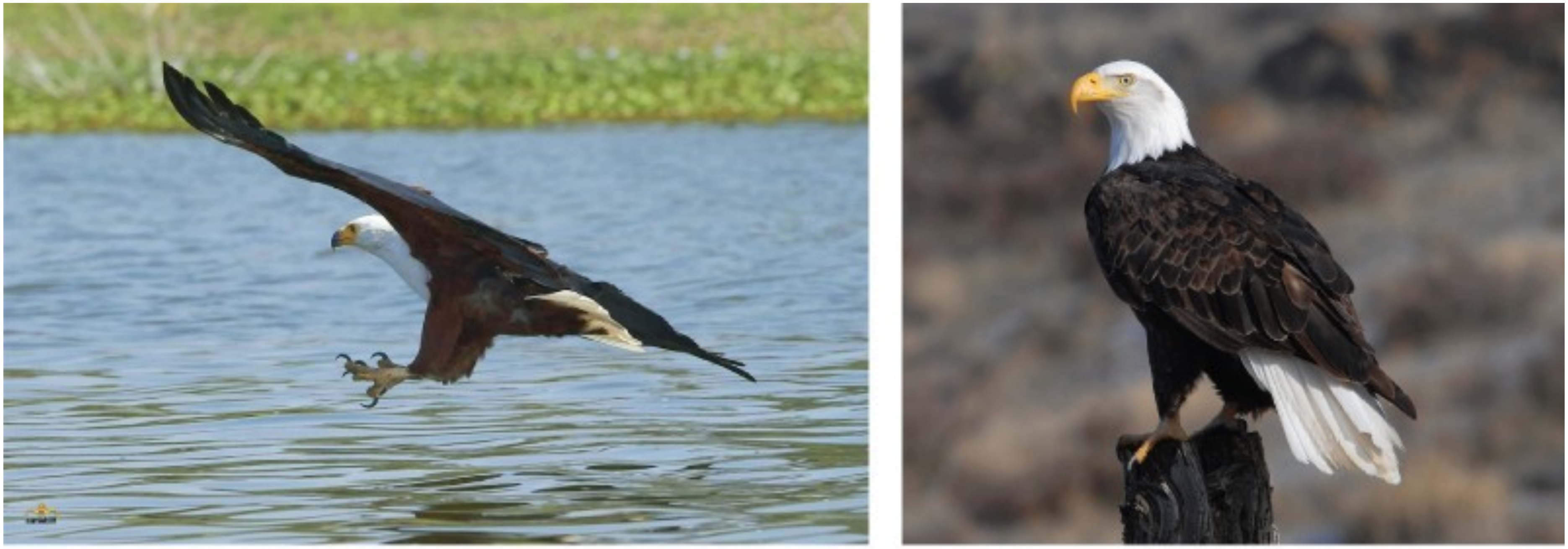






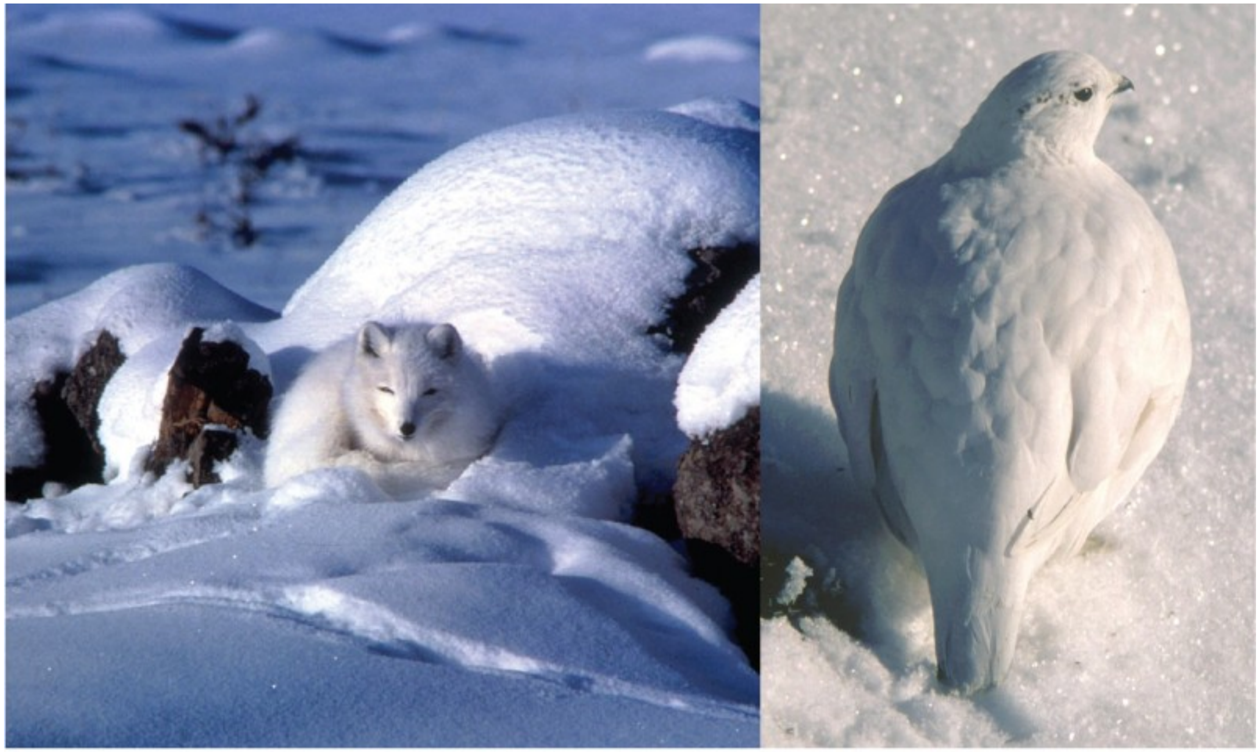
PANGOLIN

FIGURE 18.10


(a) (b)

The (a) African fish eagle is similar in appearance to the (b) bald eagle, but the two birds are members of different species. (credit a: modification of work by Nigel Wedge; credit b: modification of work by U.S. Fish and Wildlife Service)

FIGURE 18.8


(a) (b)

The white winter coat of the (a) arctic fox and the (b) ptarmigan’s plumage are adaptations to their environments. (credit a: modification of work by Keith Morehouse)

ARTIFICIAL SELECTION: SELECTIVE BREEDING

Programs and procedures designed to modify traits in domesticated species

Darwin observed pigeon breeders

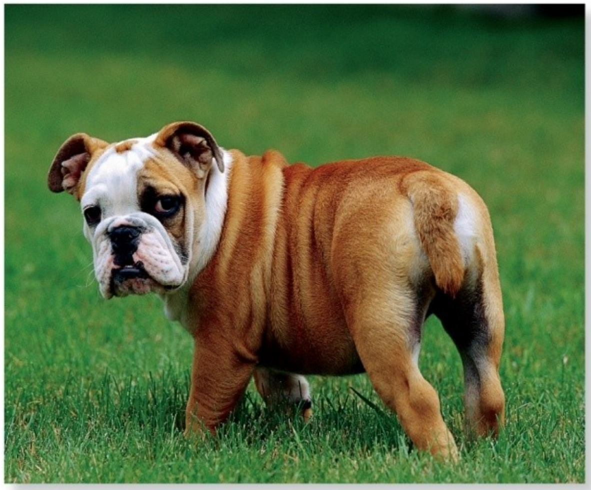
Natural selection=nature chooses those successful at surviving and reproducing

Artificial selection=humans choose who lives and reproduces

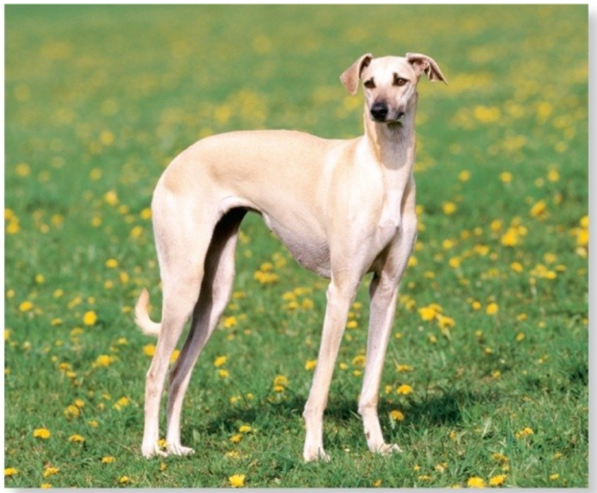
Made possible by intraspecific genetic variation

Breeders choose desirable **phenotypes**

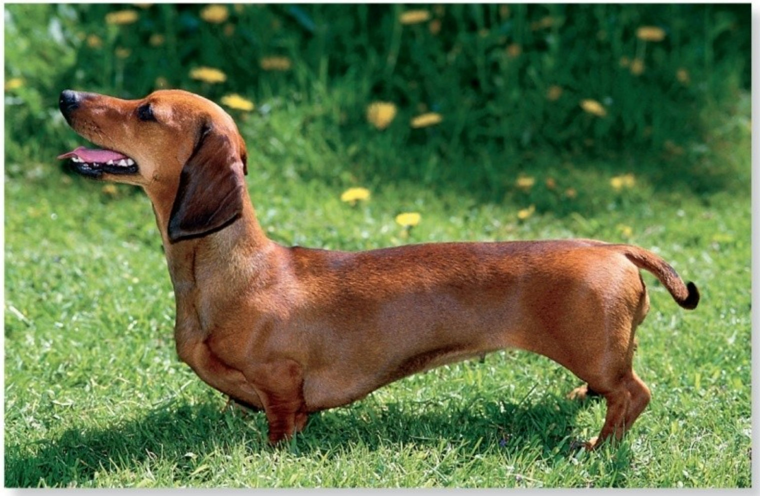
ex: **dog breeds, *Brassica* plants**, and **corn**



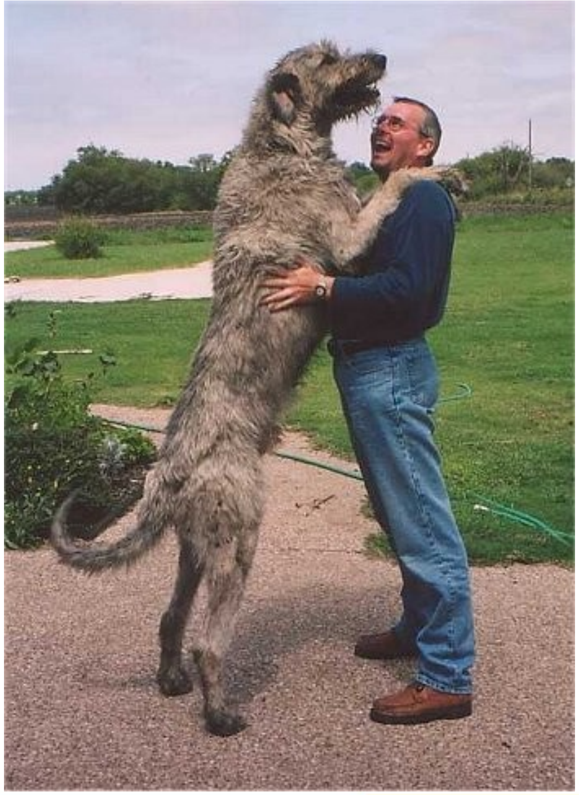
(a) Bulldog

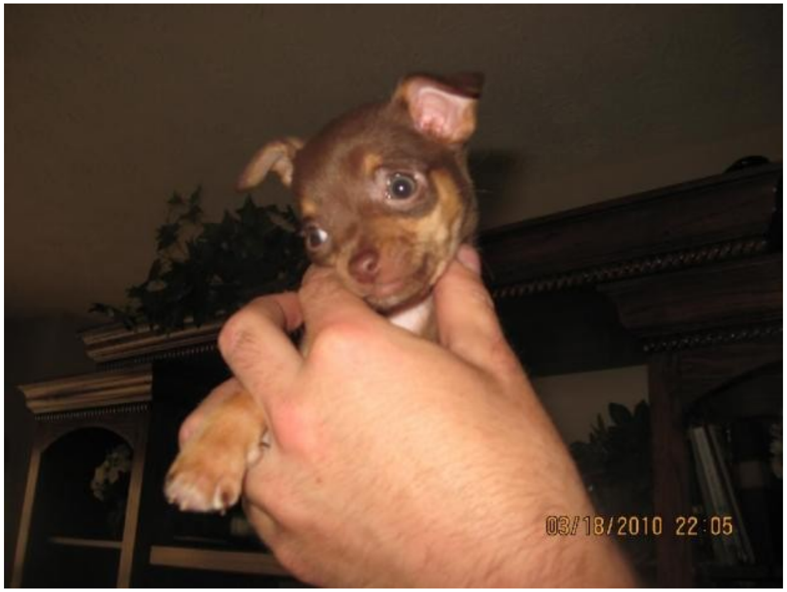


(b) Greyhound

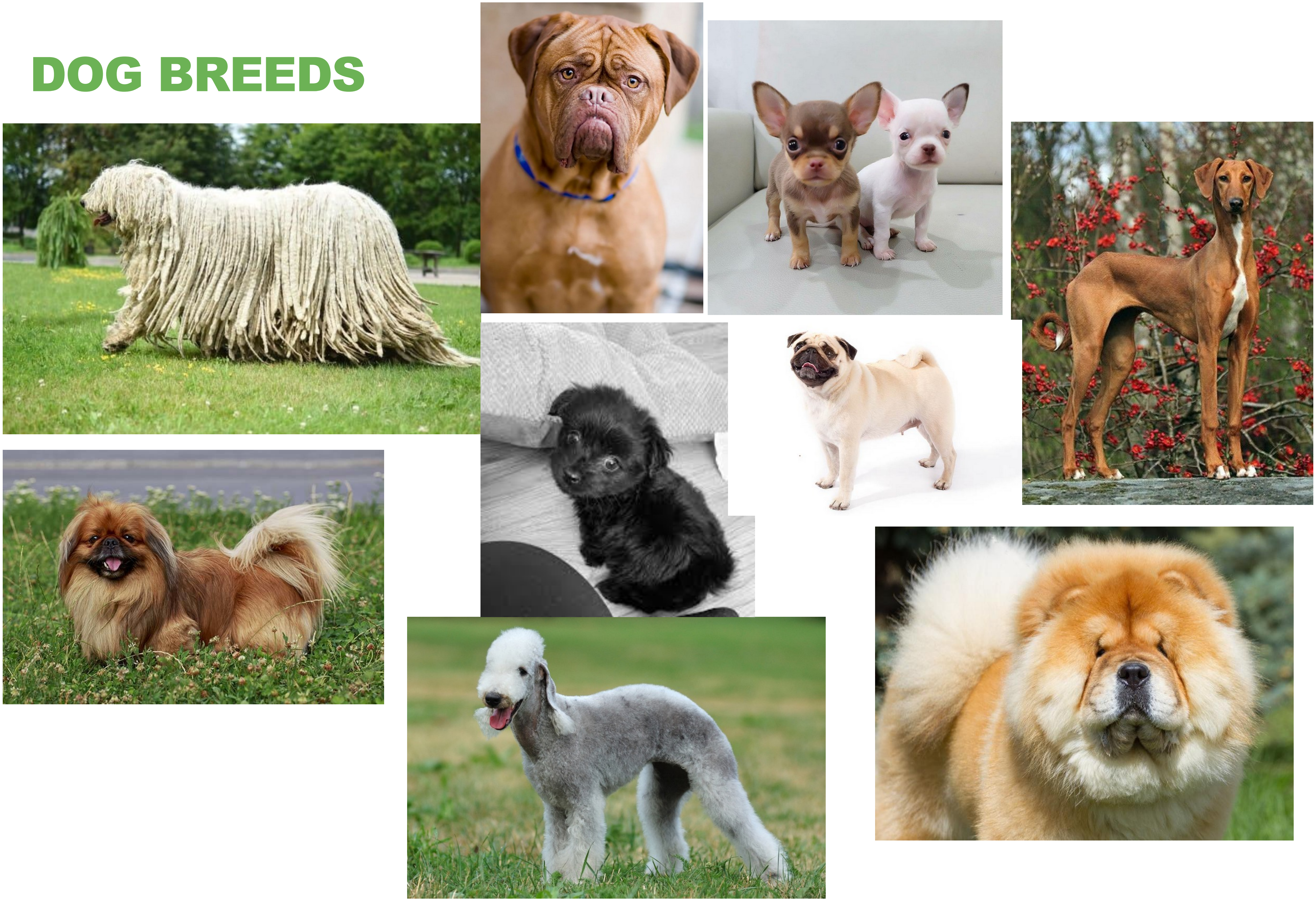


(c) Dachshund

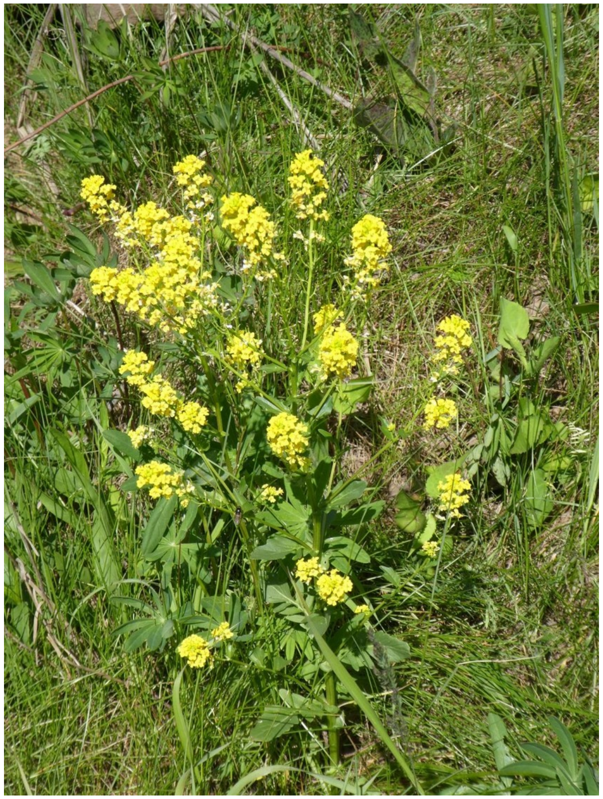




DOG BREEDS



PLANT SELECTIVE BREEDING



Wild mustard

Kohlrabi - stem

Kale - leaf

Broccoli – flower bud

Brussel sprouts – lateral leaf buds

Cabbage – terminal bud

Cauliflower – flower buds

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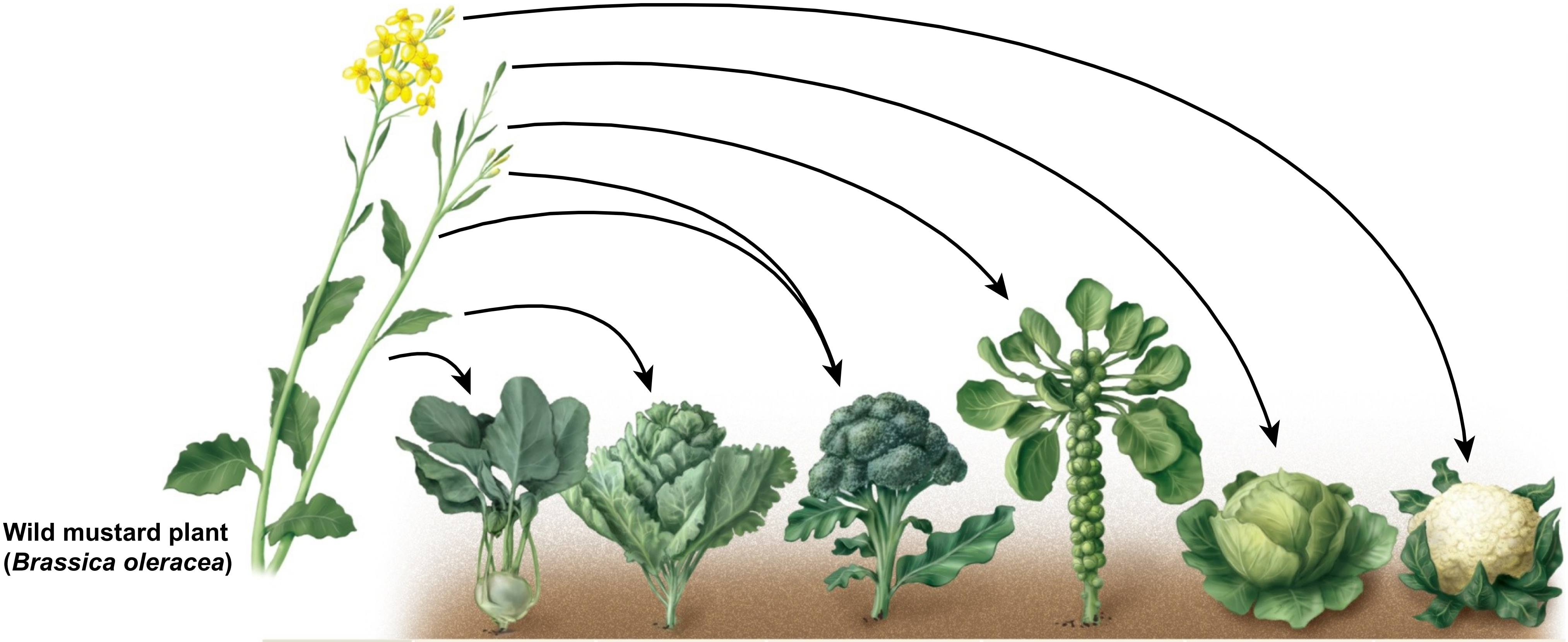


Strain	**Kohlrabi**	**Kale**	**Broccoli**	**Brussels sprouts**	**Cabbage**	**Cauliflower**
Modified trait	**Stem**	**Leaves**	**Flower buds and stem**	**Lateral leaf buds**	**Terminal leaf bud**	**Flower buds**

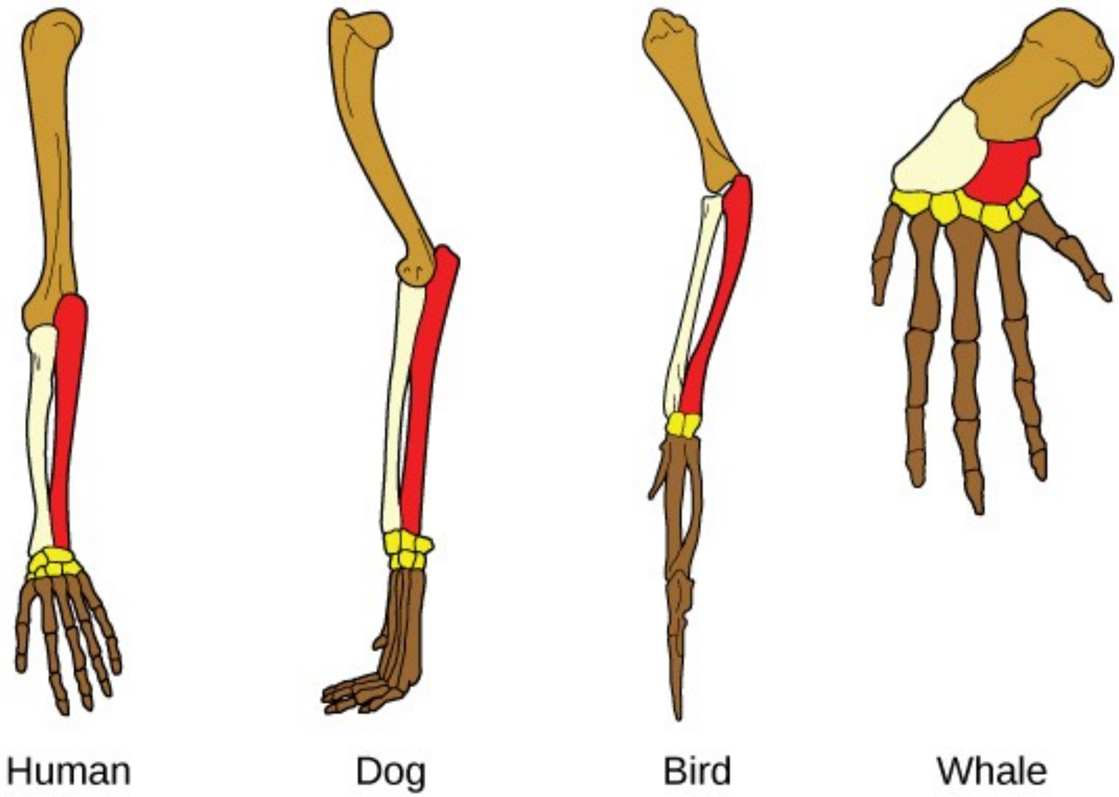
HOMOLOGY

Fundamental similarity due to
descent from a common ancestor

Homology may be

- **Anatomical**
- **Developmental**
- **Molecular**

FIGURE 18.7



The similar construction of these appendages indicates that these organisms share a common ancestor.

ANATOMICAL HOMOLOGY

Same set of bones in the limbs of modern vertebrates has undergone evolutionary change for many different purposes

Homologous structures are derived from a common ancestor

Vestigial structures are anatomical structures that have no apparent function but resemble structures of presumed ancestors

- Ear wiggling muscles

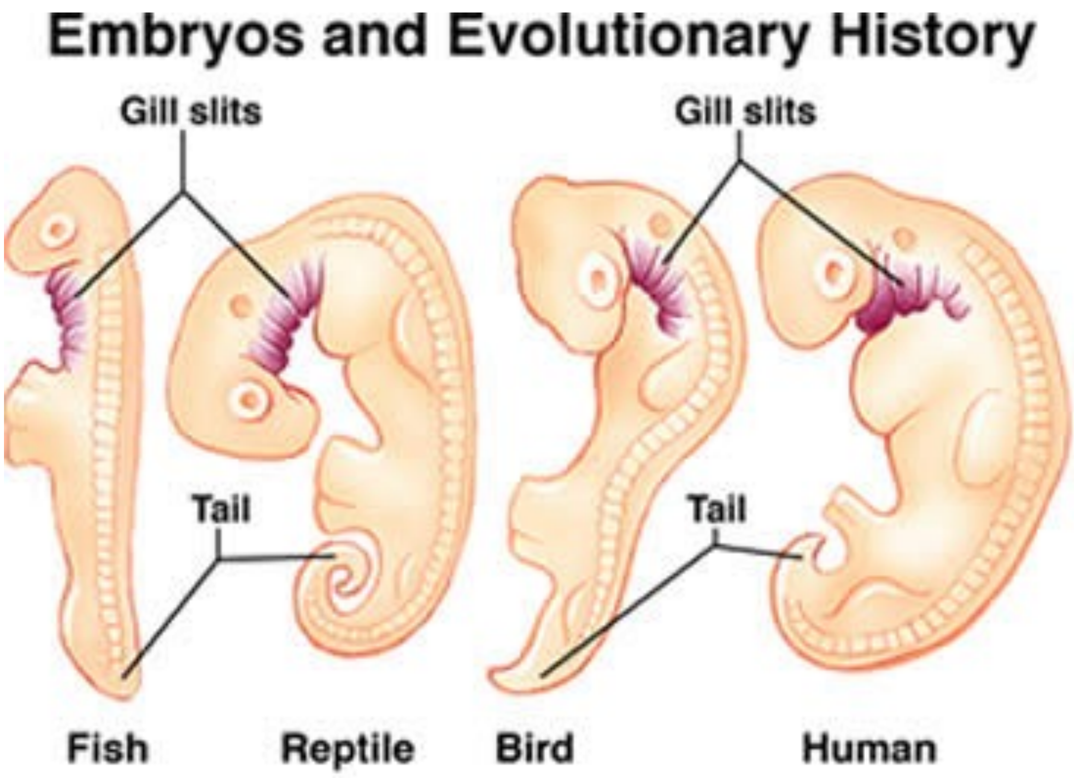
EAR WIGGLING

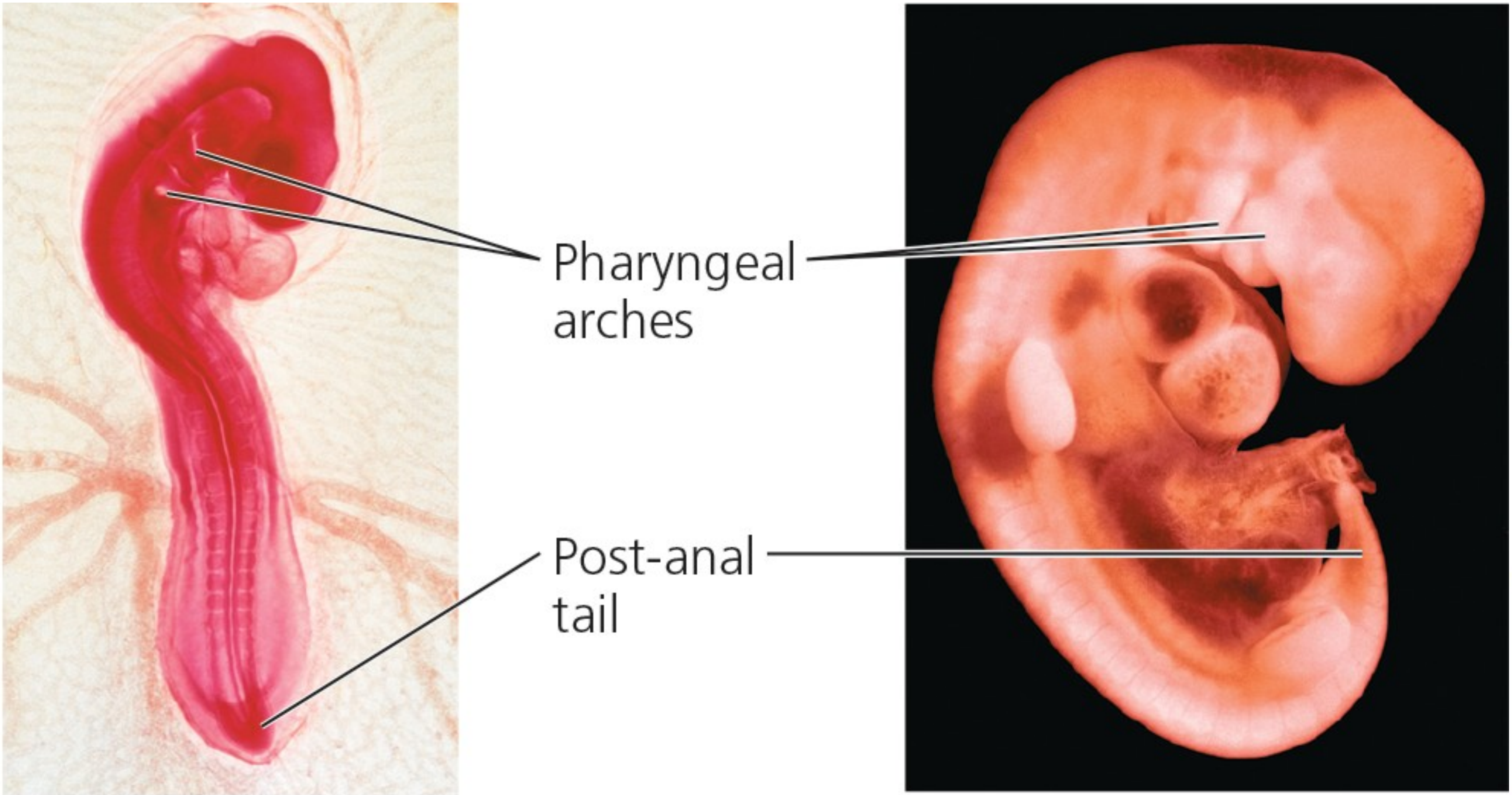
DEVELOPMENTAL HOMOLOGY

Species that differ as adults often bear striking similarities during embryonic stages

Presence of **gill ridges in human embryos** indicates that humans evolved from an aquatic animal with gill slits

Human embryos have long bony tails





Chick embryo (LM)

Human embryo

MOLECULAR HOMOLOGY

Similarities in cells at the molecular level show that living species evolved from a common ancestor

All living species use DNA to store information

Certain **biochemical pathways** are found in all or nearly all species

HORIZONTAL GENE TRANSFER

Exchange of genetic material among different species

Surprisingly common phenomenon

Can transfer

- ☐ From prokaryotes to eukaryotes
- ☐ From eukaryotes to prokaryotes
- ☐ Between prokaryotes
- ☐ Between eukaryotes

Widespread among bacteria (endosymbiosis)

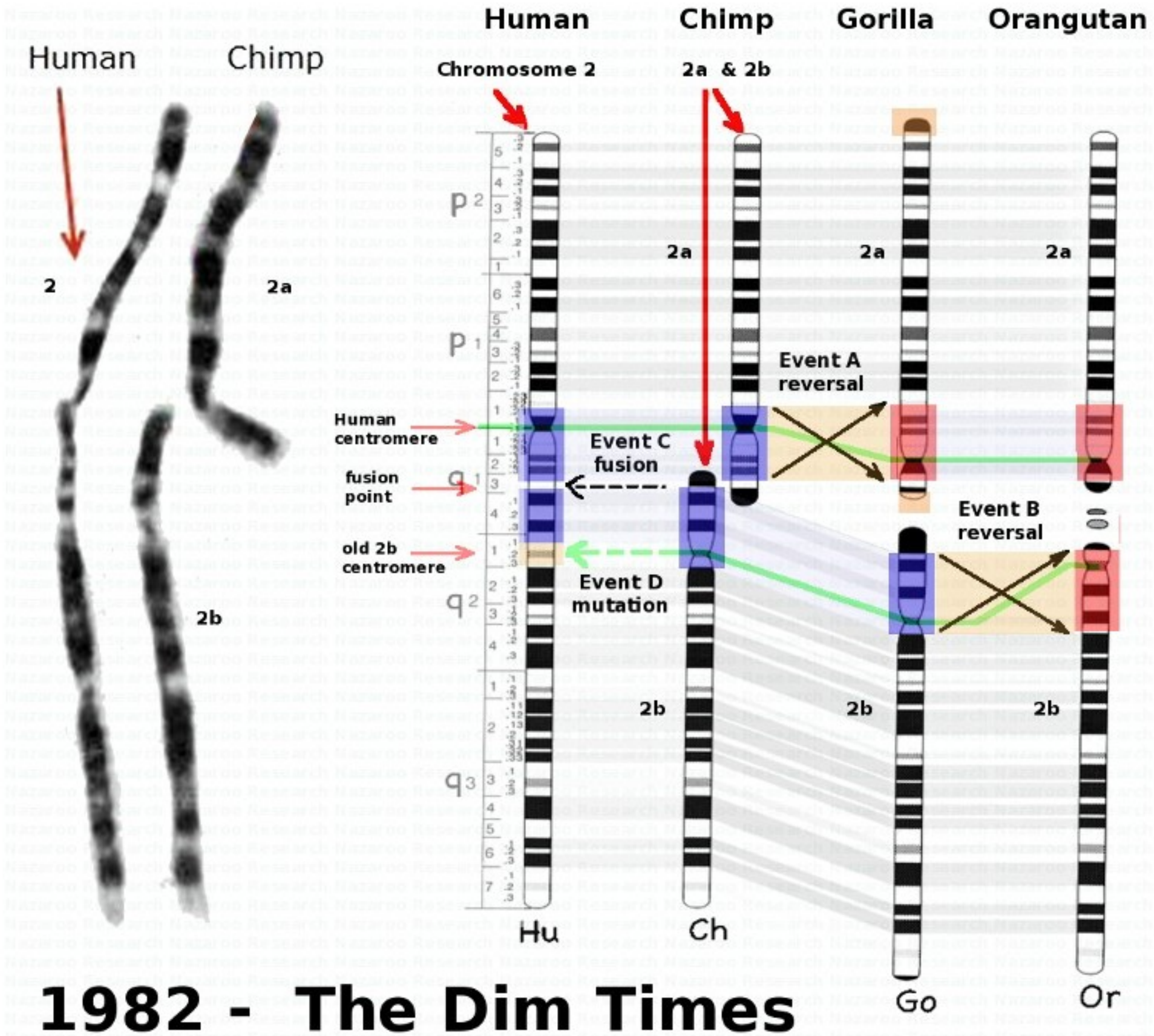
GENOMIC EVOLUTION

Evolution also occurs **at the genomic level** involving changes in chromosome structure and number

Compare three largest chromosomes in humans and apes

- Similar due to close evolutionary relationship
- Humans have one large chromosome #2 while apes have it divided into two separate chromosomes
- Chromosome 3 very similar but orangutans have a large inversion
  - May have established orangutans as a new species

Human chromosome 2



Nazaroo Research

1982 - The Dim Times

From Yunis & Prakash, Science, 1982, p 215 (1525-1530)

Mechanisms of Speciation

- Underlying cause of speciation is the **accumulation of genetic changes**
- These changes ultimately create enough differences so that we judge a population to constitute a unique species

Patterns of speciation

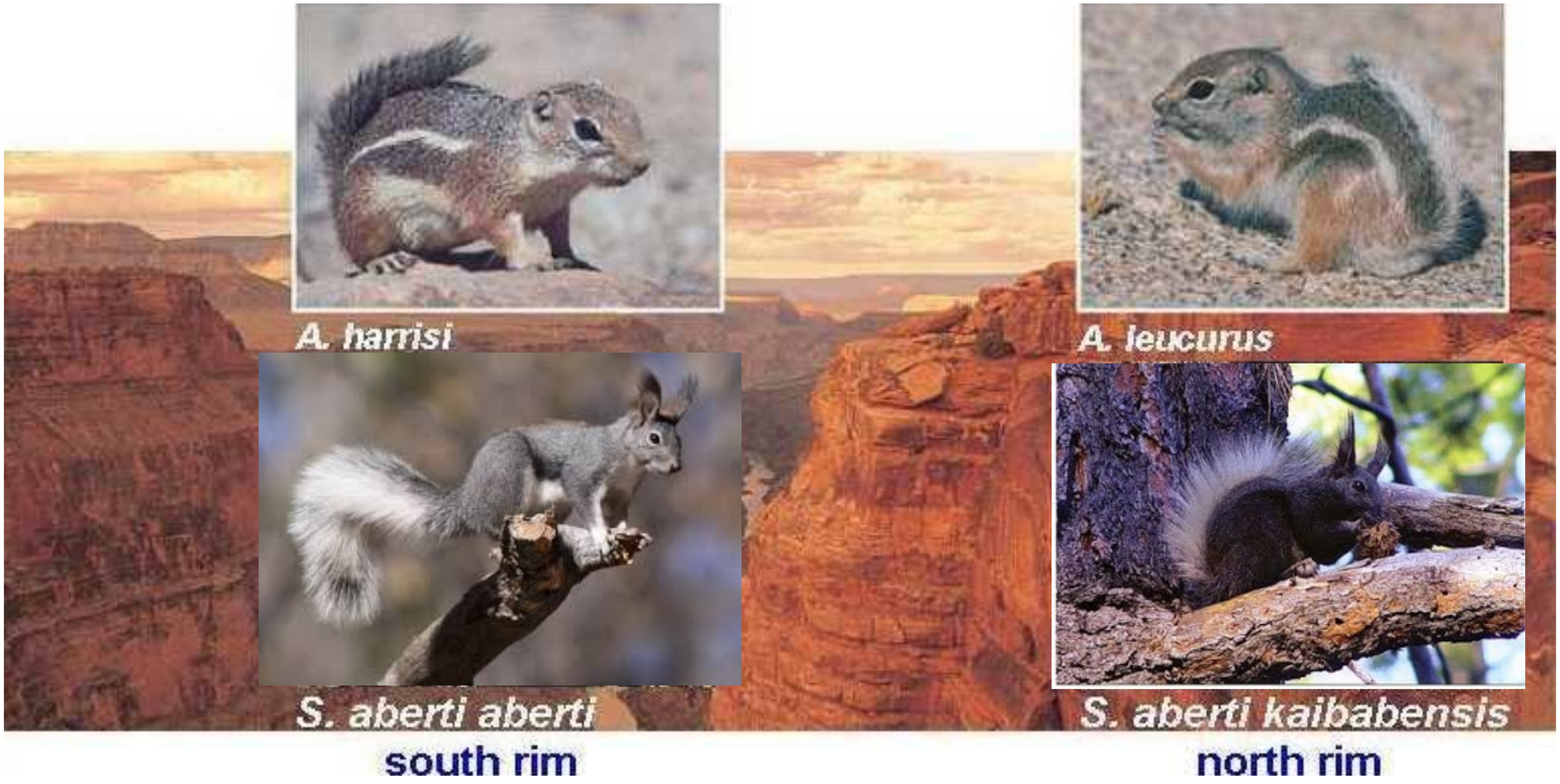
- **Cladogenesis** (formal term for speciation)
  - Division of a species into two or more species
  - Requires gene flow between populations to be **interrupted**

Methods

- **Allopatric speciation**
  - Most prevalent method for cladogenesis
  - Occurs when some members of a species become **geographically** separated

Allopatric speciation of squirrels (10,000 ya) in the Grand Canyon

Antelope squirrels: (*Ammospermophilus*) Harris and white-tailed



Tassel-eared squirrels: (*Sciurus*) Abert’s squirrel and Kaibab squirrel

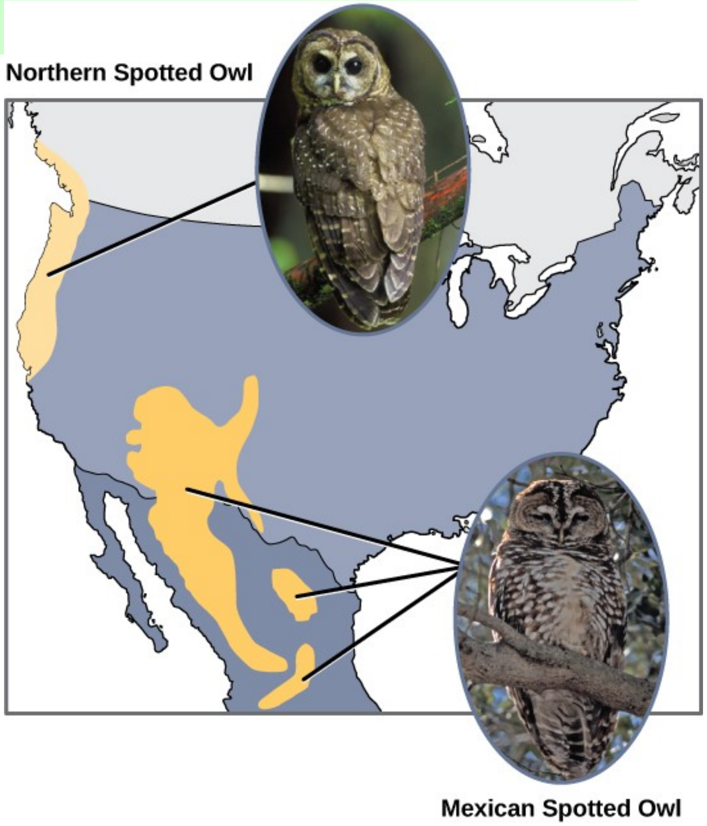
Grand Canyon Formation

Reproductive isolating mechanisms

- Mechanisms that prevent interbreeding between different species
- Consequence of genetic changes as species evolutionarily adapts to its environment
- **Interspecies hybrid** – when two species do produce offspring

Prezygotic barriers

- **Habitat isolation**
  - ❑Geographic barrier prevents contact
  - ❑Allopatric speciation



The northern spotted owl and the Mexican spotted owl inhabit geographically separate locations with different climates and ecosystems. The owl is an example of incipient speciation (new species have formed but are still capable of interbreeding) (credit "northern spotted owl": modification of work by John and Karen Hollingsworth; credit "Mexican spotted owl": modification of work by Bill Radke)

a: © C. Allan Morgan/Getty Images; b: © Bryan E. Reynolds

- **Habitat isolation**

Populations of a species move or are moved to a new habitat and take up residence in a place that no longer overlaps with the other populations of the same species.

(a) *Gryllus pennsylvanicus* prefers sandy soil.

(b) *Gryllus firmus* prefers loamy soil.

- **Temporal isolation**
  - ❑Reproduce at different times of the day or year

- These two related frog species exhibit temporal reproductive isolation. (a) *Rana aurora* breeds earlier in the year than (b) *Rana boylii*. (credit a: modification of work by Mark R. Jennings, USFWS; credit b: modification of work by Alessandro Catenazzi)
- Temporal Isolation is reproduction at separate times of year.

- **Behavioral isolation**
  - Behaviors important in mate choice
  - ex: [Changes in song]

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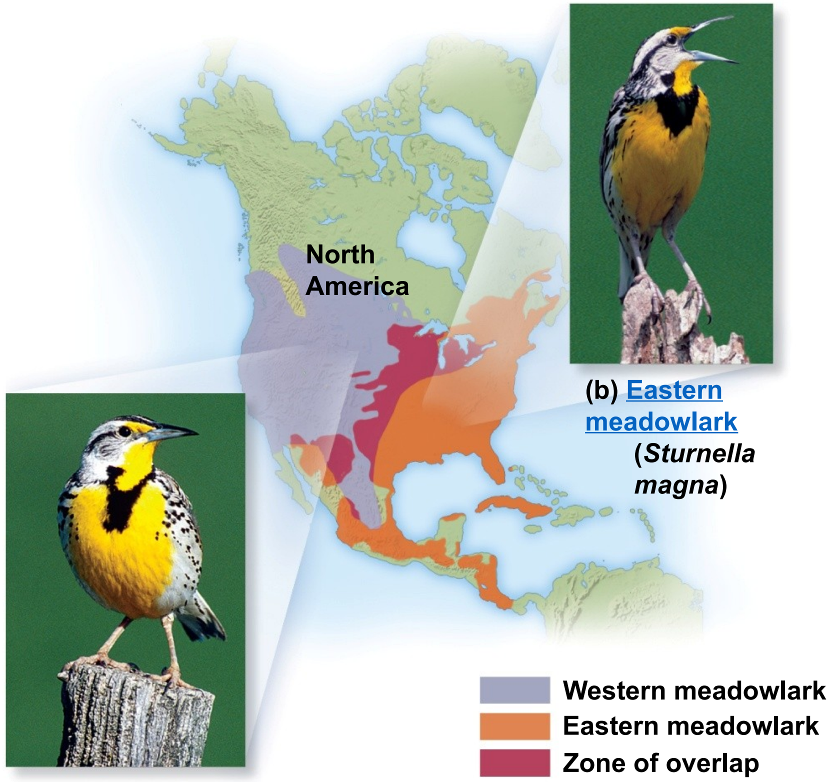
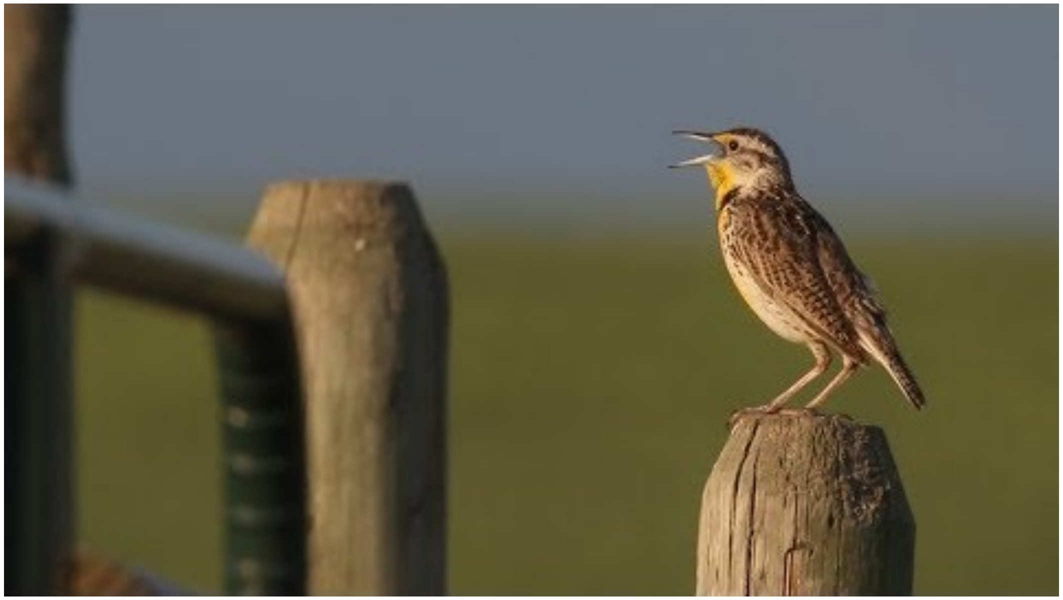


(a) [Western meadowlark] (***Sturnella neglecta***)

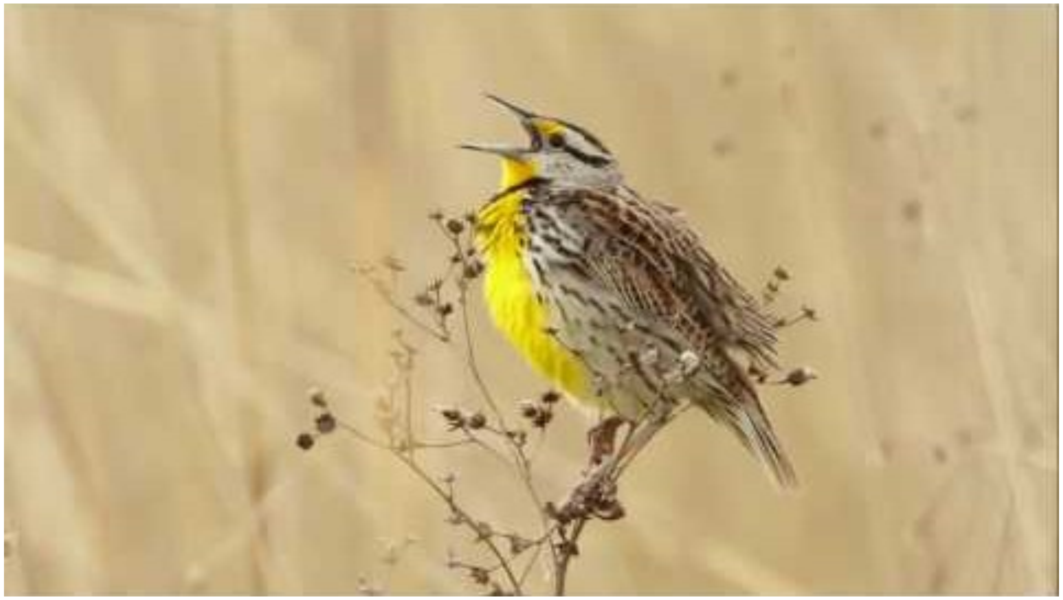
(b) [Eastern meadowlark] (***Sturnella magna***)

a: © Rod Planck/Photo Researchers, Inc.; b: © Ron Austing/Photo Researchers, Inc.

Western meadowlark



Eastern Meadowlark



Courtship rituals as behavioral isolating mechanisms

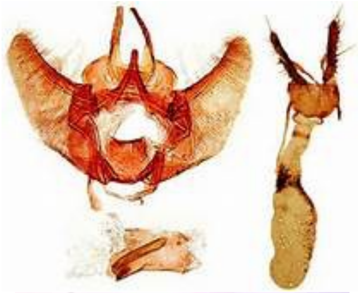
Courtship ritual as a behavioral barrier between species: Blue footed boobies (3:08), Manakins (1:50) Bowerbirds (2:07)

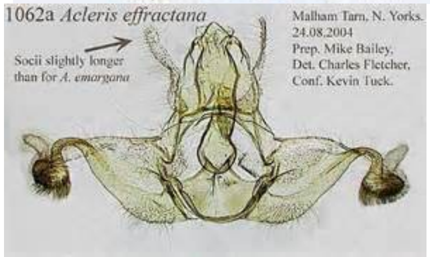
Manakins

Bowerbirds

Blue Footed Booby

- **Mechanical isolation**
  - ❑Size or incompatible genitalia prevents mating





- **Gametic isolation**
  - ❑Gametes fail to unite
  - ❑Important in species that release gametes into the water or air

Postzygotic barriers

- **Postzygotic barriers**
  - Block development of viable, fertile individuals
  - Less common in nature because they are more costly in terms of energy and resources used

Postzygotic barriers

- **Postzygotic barriers**
    - ❑Block development of viable, fertile individuals
    - ❑Less common in nature because they are more costly in terms of energy and resources used

- **Hybrid inviability** – fertilized egg cannot progress past an early embryo

- **Hybrid sterility** – interspecies hybrid viable but sterile
    - ❑Mule

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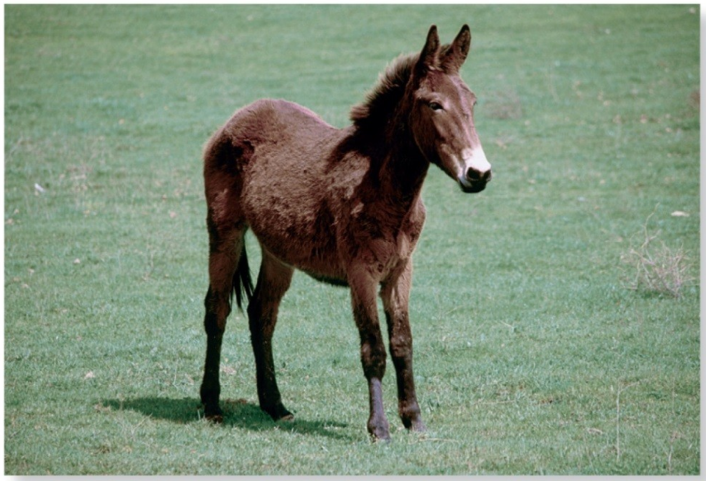
Male donkey (*Equus asinus*)

×

Female horse (*Equus ferus caballus*)



Mule

(top left): © Mark Boulton/Photo Researchers, Inc.; (top right): © Carolina Biological Society/Visuals Unlimited;
(bottom): © Stephen L. Saks/Photo Researchers, Inc.

Postzygotic barriers

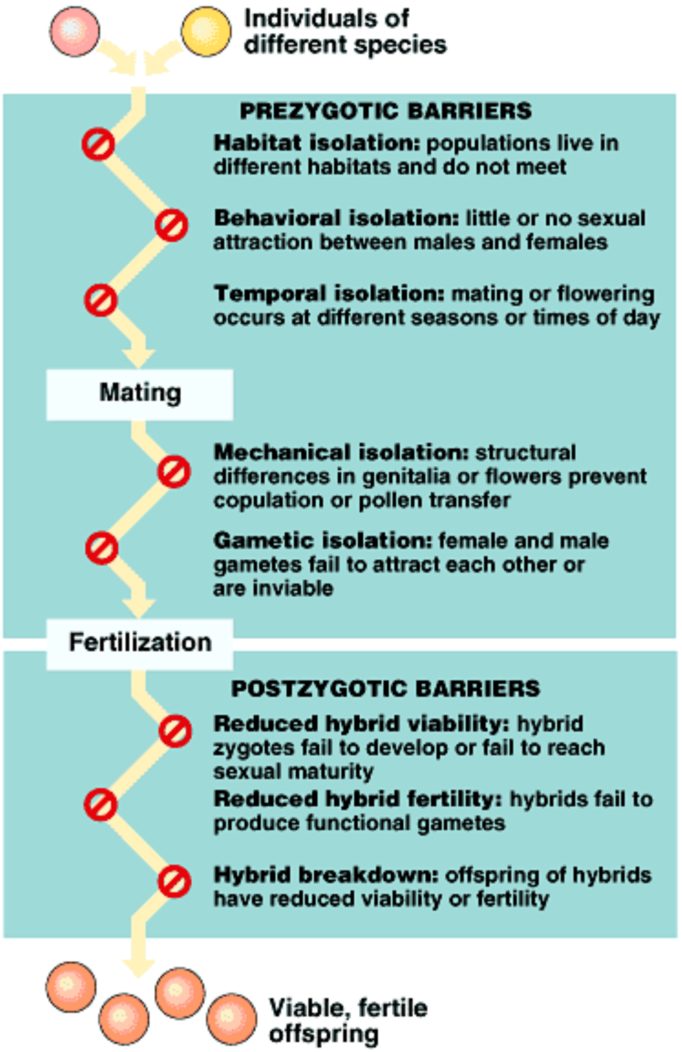
- **Postzygotic barriers**
    - ❑Block development of viable, fertile individuals
    - ❑Less common in nature because they are more costly in terms of energy and resources used

- **Hybrid inviability** – fertilized egg cannot progress past an early embryo

- **Hybrid sterility** – interspecies hybrid viable but sterile
    - ❑Mule

❑**Hybrid breakdown** – hybrids viable and fertile but subsequent generations have genetic abnormalities and are not fertile. Most common in plants. Cotton varieties

A summary of reproductive barriers between closely related species



PREZYGOTIC BARRIERS

Habitat isolation: populations live in different habitats and do not meet

Behavioral isolation: little or no sexual attraction between males and females

Temporal isolation: mating or flowering occurs at different seasons or times of day

Mechanical isolation: structural differences in genitalia or flowers prevent copulation or pollen transfer

Gametic isolation: female and male gametes fail to attract each other or are inviable

POSTZYGOTIC BARRIERS

Reduced hybrid viability: hybrid zygotes fail to develop or fail to reach sexual maturity

Reduced hybrid fertility: hybrids fail to produce functional gametes

Hybrid breakdown: offspring of hybrids have reduced viability or fertility

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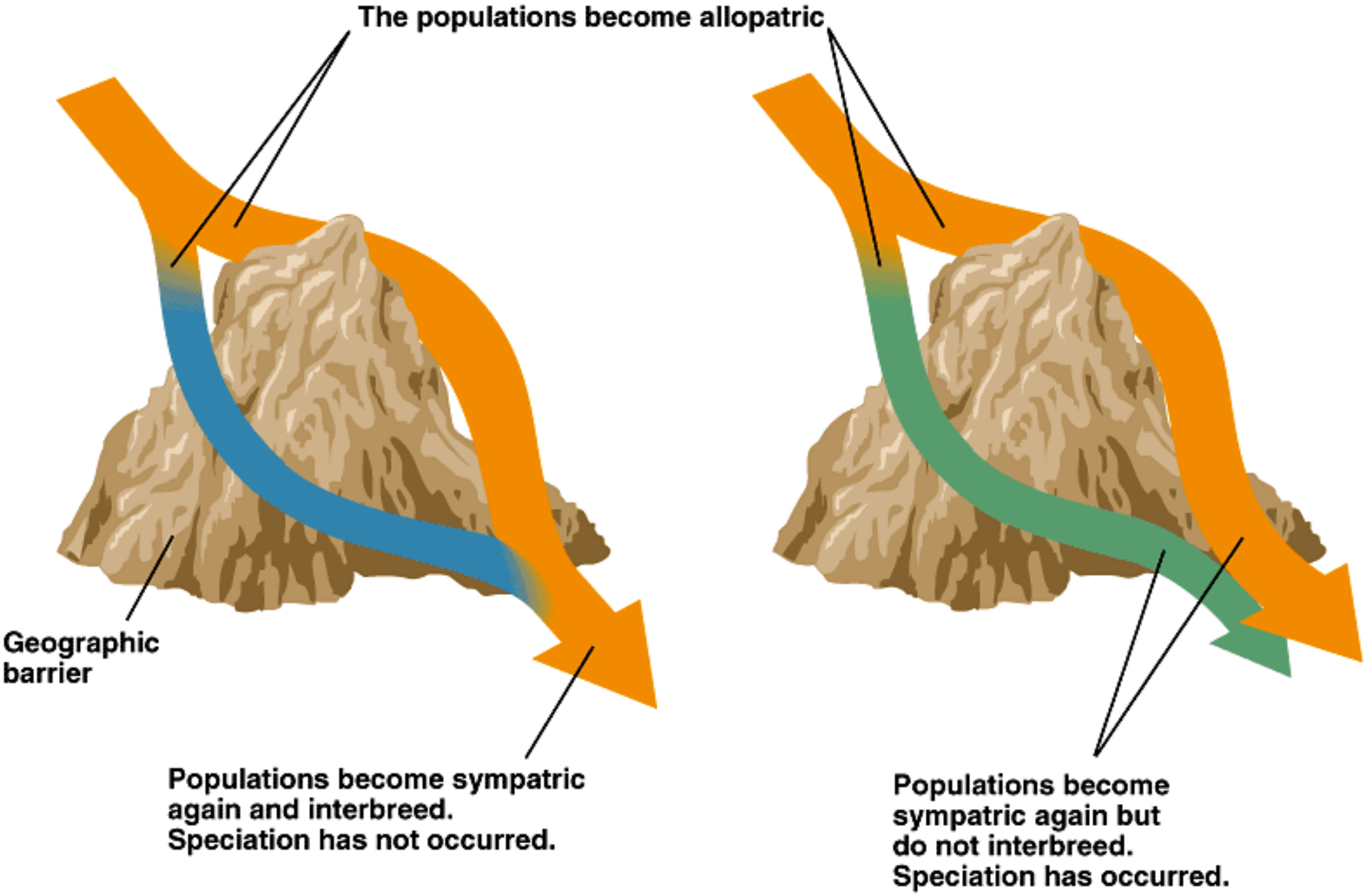
After allopatric speciation

- 1. Prezygotic barriers
  - Reproductive isolating mechanisms
    - Habitat isolation
    - Temporal isolation
    - Behavioral isolation
    - Mechanical isolation
    - Gametic isolation
- 2. Postzygotic barriers
  - Hybrid inviability
  - Hybrid sterility
  - Hybrid breakdown

Mechanisms of Speciation

- Underlying cause of speciation is the **accumulation of genetic changes** that ultimately promote enough differences so that we judge a population to constitute a unique species

Has speciation occurred during geographic isolation?



The populations become allopatric

Geographic barrier

Populations become sympatric again and interbreed. Speciation has not occurred.

Populations become sympatric again but do not interbreed. Speciation has occurred.

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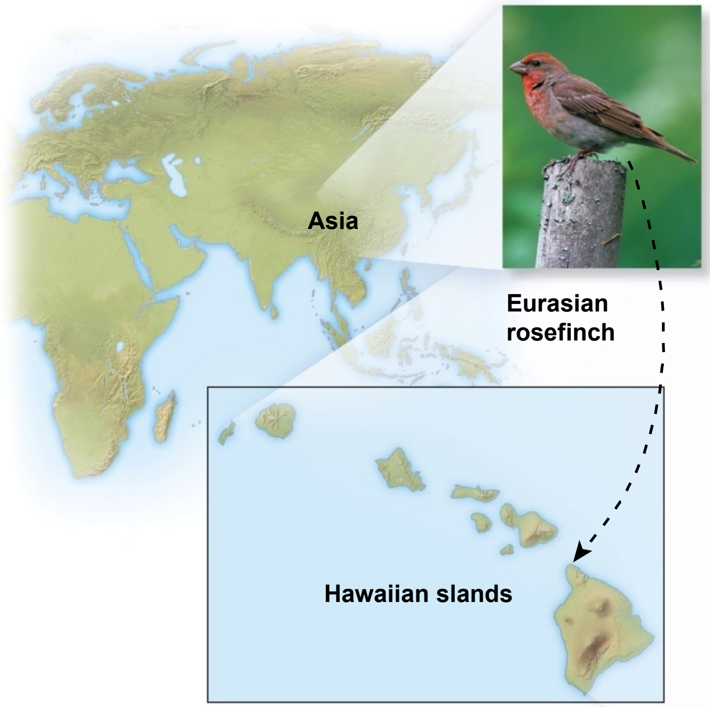
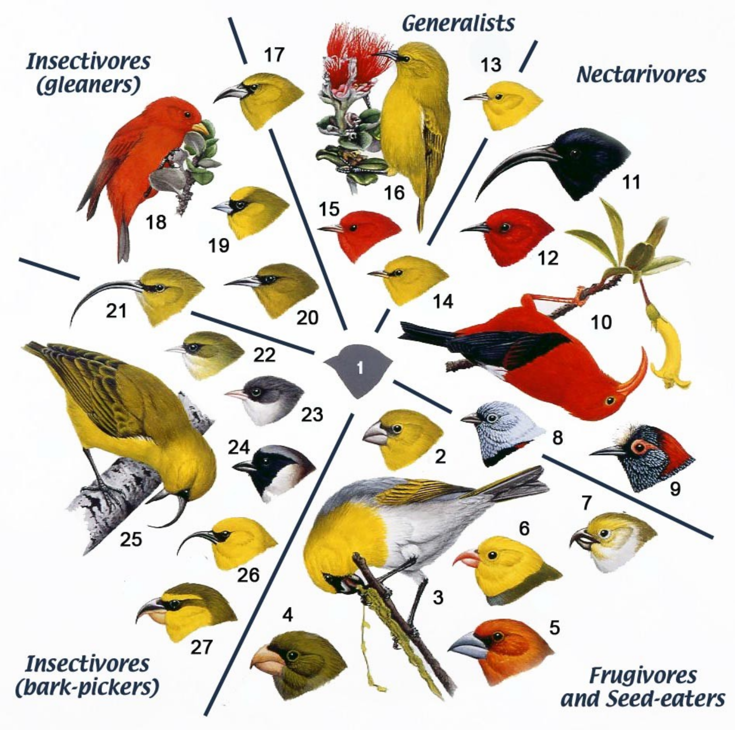
Speciation and Adaptive radiation

- Can also occur when a small population moves to a new location that is geographically separated
  - **Natural selection** may rapidly alter the genetic composition of the population, leading to adaptation to the new environment
  - **Adaptive radiation** – single species evolves into array of descendants that differ greatly in habitat, form or behavior (Darwin’s finches)



Migration of ancestor to the Hawaiian Islands



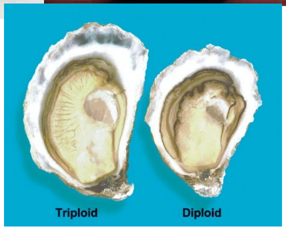
The honeycreeper birds illustrate adaptive radiation. From one original species of bird, multiple others evolved, each with its own distinctive characteristics.

Sympatric speciation

- Occurs when members of a species that are **within the same range** diverge into two or more different species even though there are no physical barriers to interbreeding

- Mechanisms include
  - ❑ **Polyploidy**
  - ❑ **Adaptation to local environments**
  - ❑ **Sexual selection**

99%



Triploid
trout

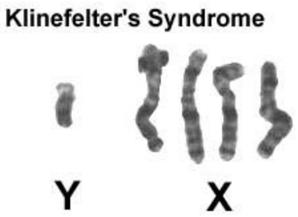
- **Polyploidy**
  - ☐ Organism has **two or more sets of chromosomes**
  - ☐ Polyploidy more frequent in plants than animals
  - ☐ Can occur through **nondisjunction** (autoploidy)
  - ☐ **Alloploids** contain chromosomes from two or more different species
  - ☐ Alloploids wheat, tobacco, cotton

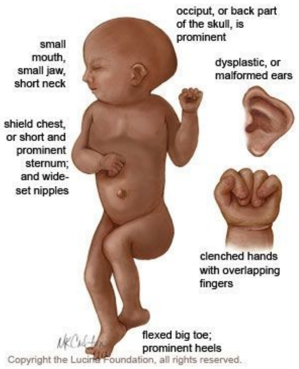
Asian water lotus

80%

Polyploidy and Aneuploidy

- The state of having more than two sets of chromosomes is called **polyploidy**.
- Aneuploidy is having the wrong number of chromosomes, either more or less.
- Many plants are polyploid, but the condition is inevitably fatal for human beings.




small mouth, small jaw, short neck
shield chest, or short and prominent sternum; and wide-set nipples
occiput, or back part of the skull, is prominent
dysplastic, or malformed ears
clenched hands with overlapping fingers
flexed big toe; prominent heels

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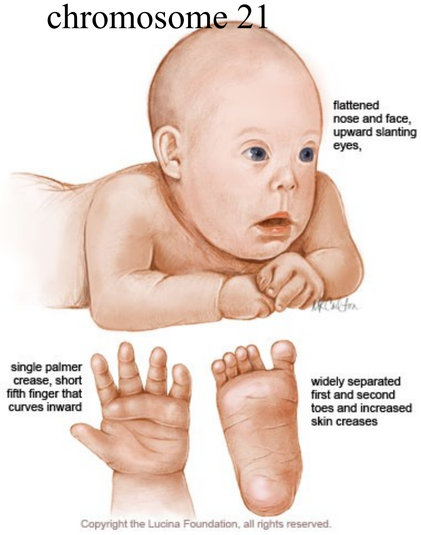
Down Syndrome, 3 copies chromosome 21


flattened nose and face, upward slanting eyes,
single palmer crease, short fifth finger that curves inward
widely separated first and second toes and increased skin creases

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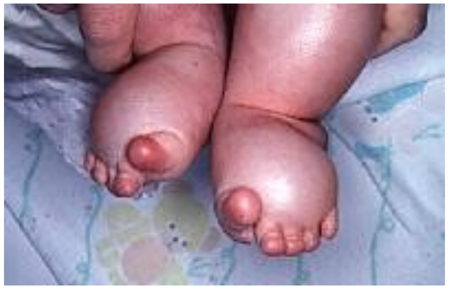
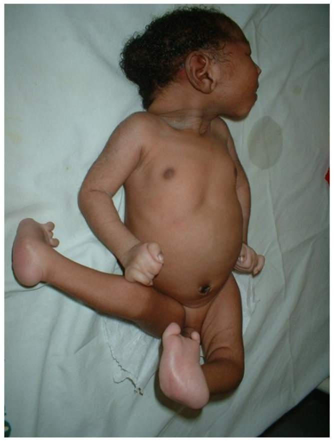
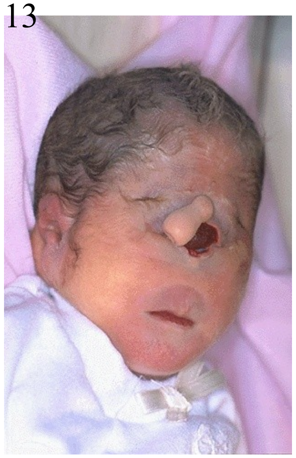
Turner's Syndrome, 1 X chromosome only



Edward's Syndrome, 3 copies chromosome 18



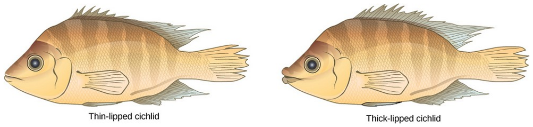
Patau Syndrome, 3 copies chromosome 13



Sympatric Speciation

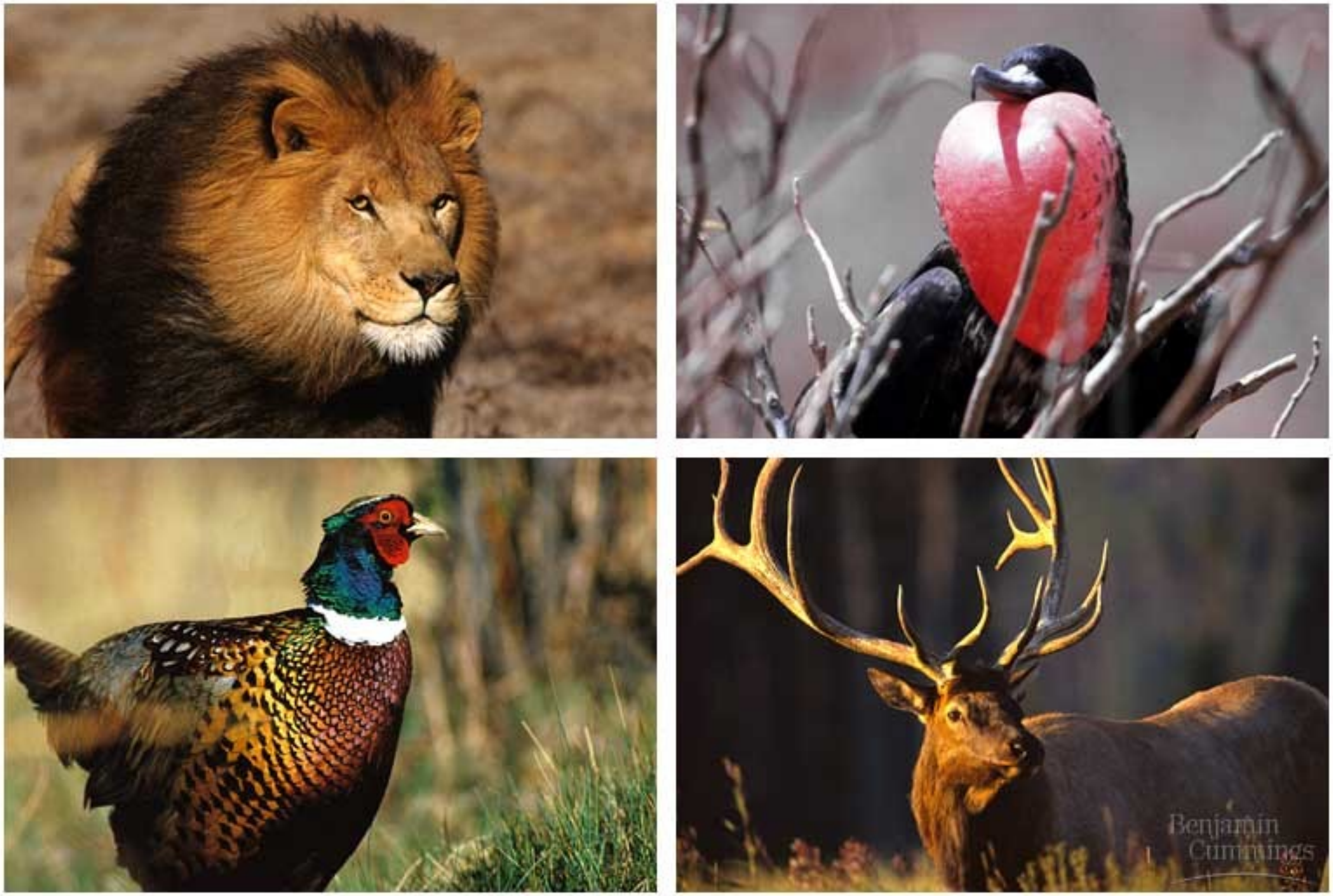
- **Adaptation to local environments**
  - Geographic area may have variation so that some members of a population may diverge and occupy different local environments that are continuous with each other
- **Sexual selection**
  - Certain females prefer males with one color pattern, while other females prefer males with a different color pattern

Figure 18.21

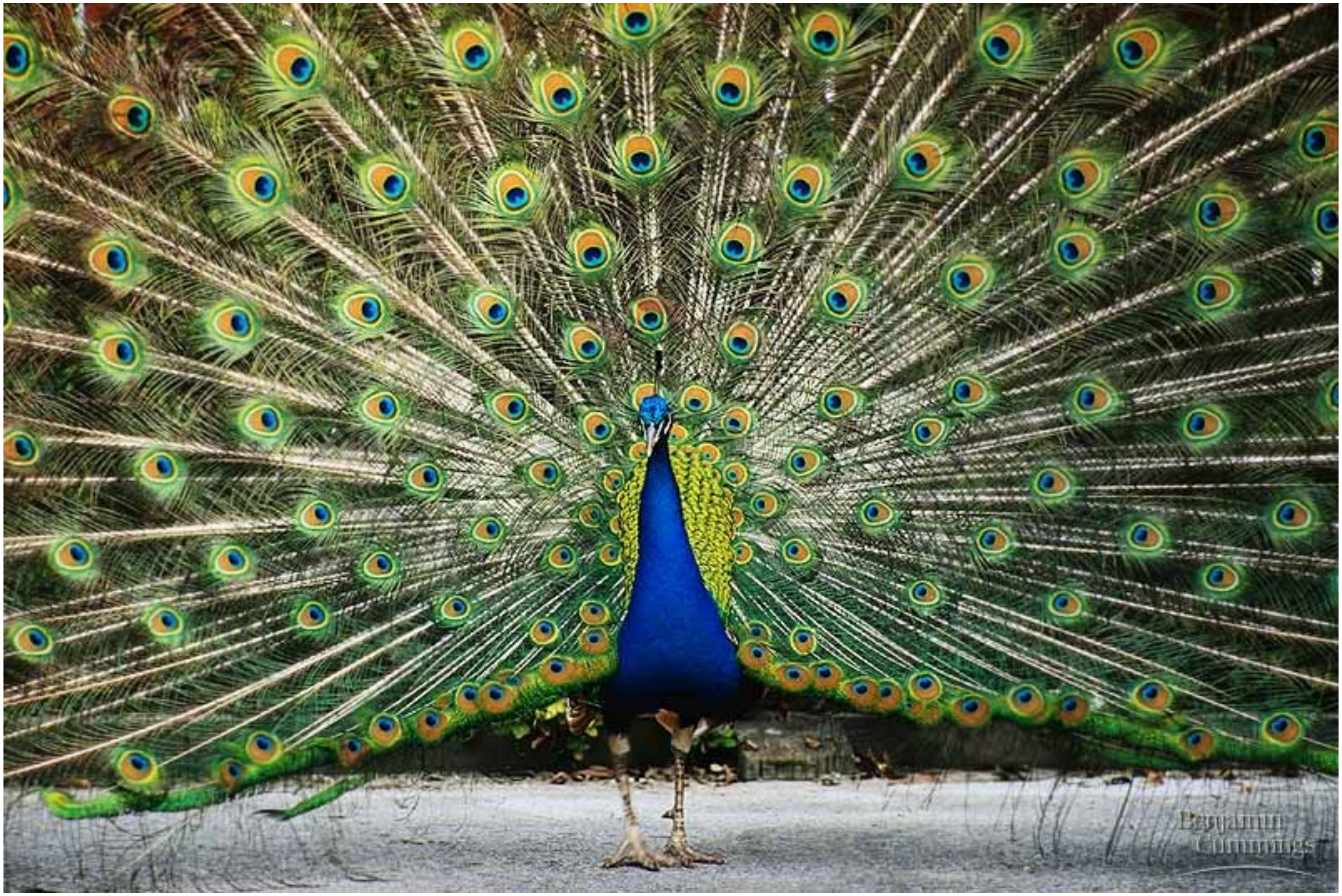


- Cichlid fish from Lake Apoyeque, Nicaragua, show evidence of sympatric speciation. Lake Apoyeque, a crater lake, is 1800 years old, but genetic evidence indicates that the lake was populated only 100 years ago by a single population of cichlid fish. Nevertheless, two populations with distinct morphologies and diets now exist in the lake, and scientists believe these populations may be in an early stage of speciation.

Sexual selection and the evolution of male appearance



Male peacock



Sympatric Speciation

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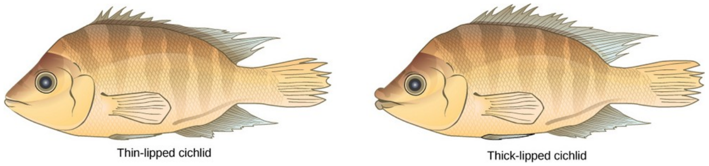
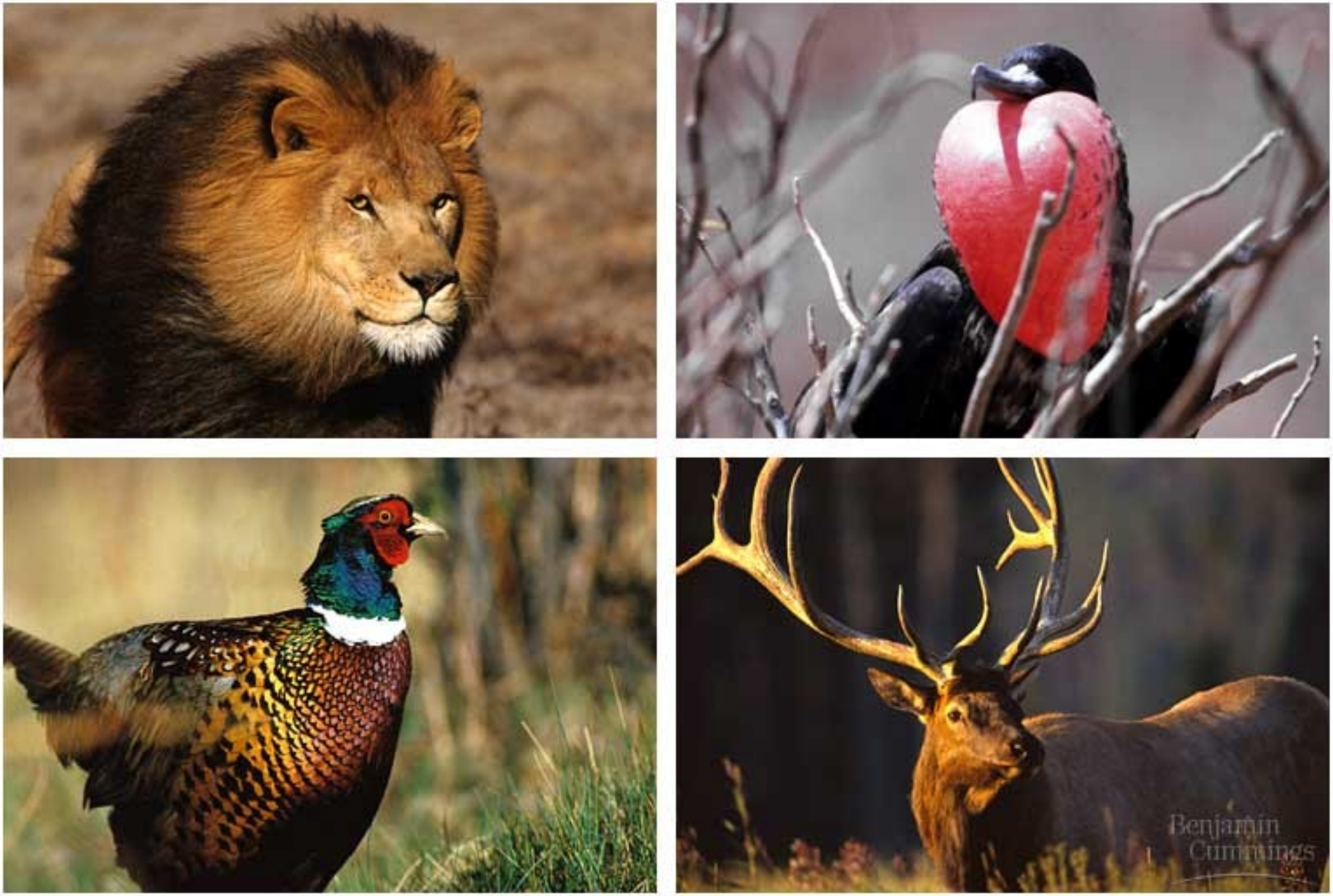
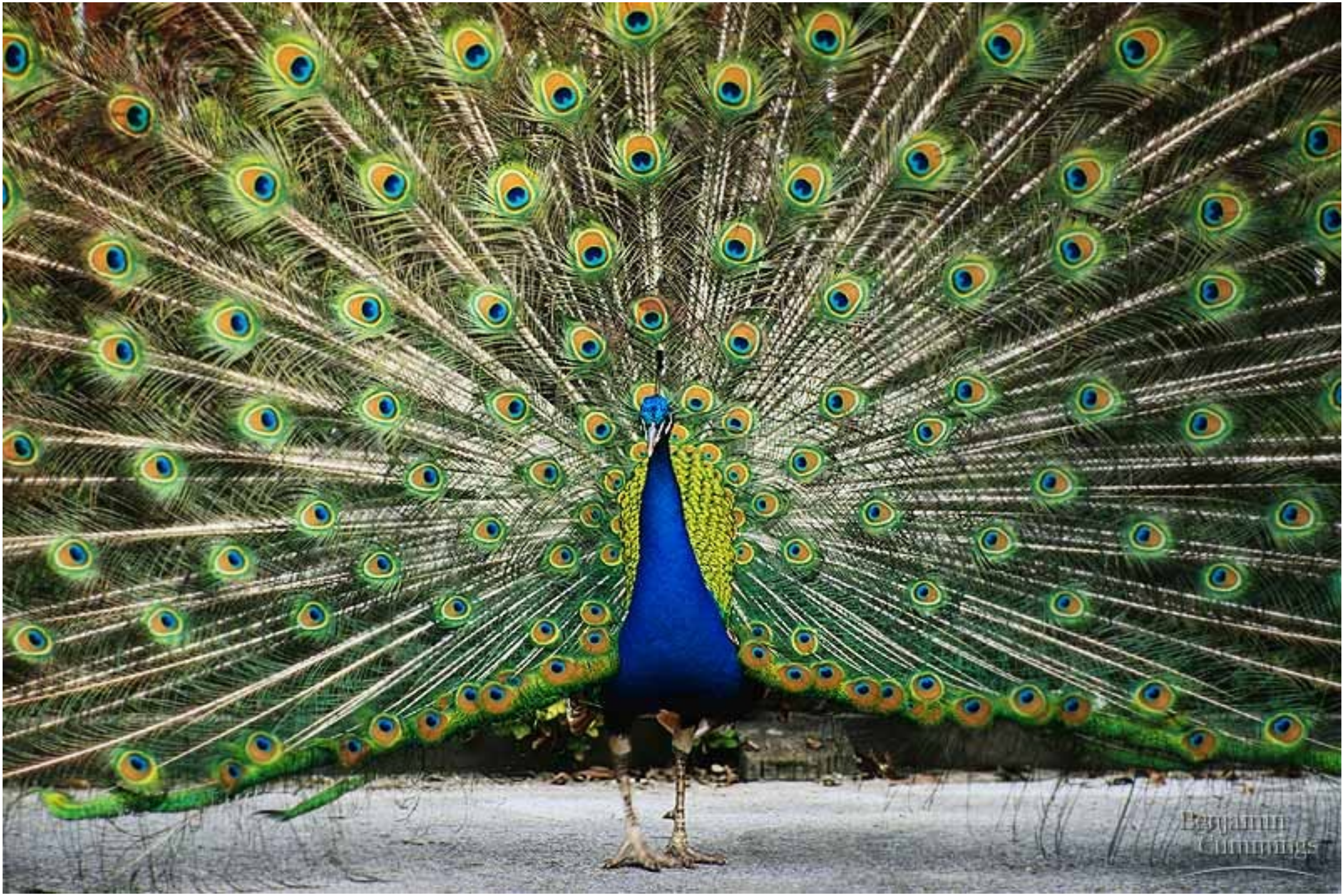


Sexual selection and the evolution of male appearance



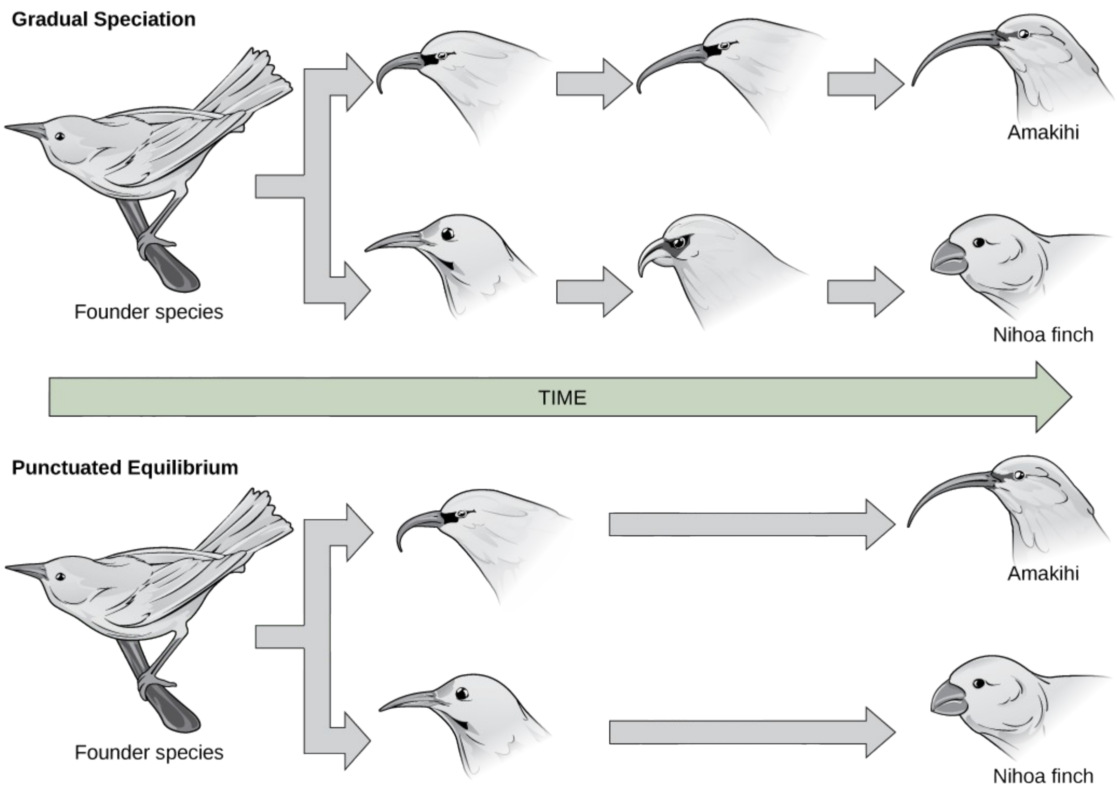
Male peacock



The Pace of Speciation

- **Gradualism**
  - ❑ Each new species evolves continuously over long spans of time
  - ❑ Large phenotypic differences that produce new species are due to the accumulation of many small genetic changes
- **Punctuated equilibrium**
  - ❑ Tempo more sporadic
  - ❑ Species in equilibrium for long periods and then short rapid bursts of changes
- Both views have merit

Figure 18.23



- In (a) gradual speciation, species diverge at a slow, steady pace as traits change incrementally. In (b) punctuated equilibrium, species diverge quickly and then remain unchanged for long periods of time.

Evo-Devo: Evolutionary Developmental Biology

27.1

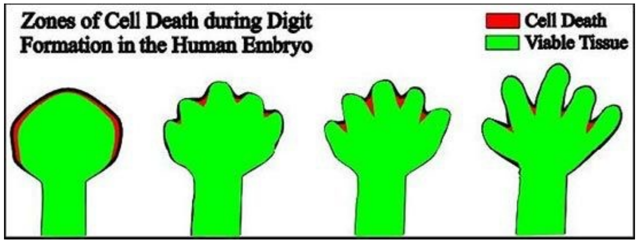
- Compares the development of different organisms to understand:
  - Ancestral relationships between organisms
  - Developmental mechanisms that bring about evolutionary change
- Involves the discovery of genes that control development, and how their roles vary in different species

Developmental genes are key

- Genes that play a role in development may influence
  - ❑ Cell division
  - ❑ Cell migration
  - ❑ Cell differentiation
  - ❑ Cell death (apoptosis)
- Interplay produces an organism with a specific body pattern (pattern formation)
- Developmental genes are very important to the phenotypes of individuals

Chicken vs. duck feet

- Differences in expression of two cell-signaling proteins
  - **BMP4** – causes cells to undergo apoptosis (programmed cell death) and die
  - **Gremlin** – inhibits the function of BMP4 and allows cell to survive


Zones of Cell Death during Digit Formation in the Human Embryo
🟥 Cell Death
🟩 Viable Tissue

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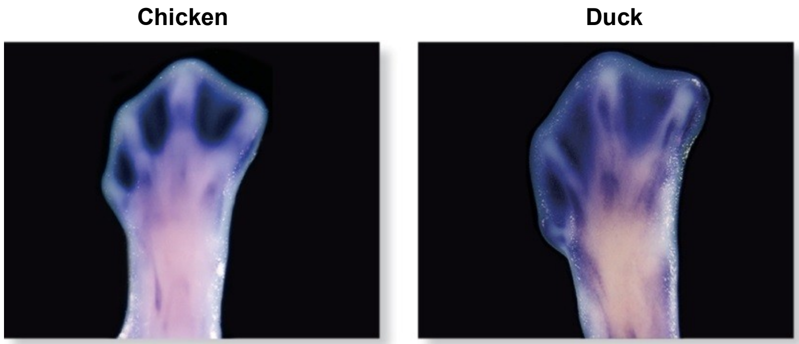
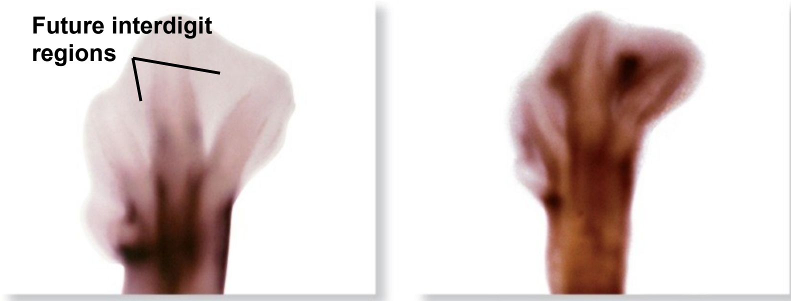
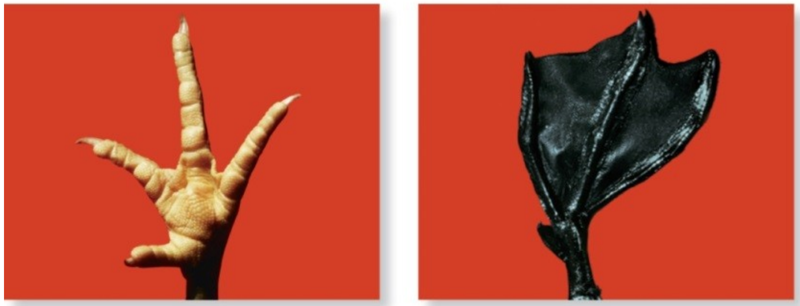


(a) BMP4 protein levels - similar expression in chicken and duck



(b) Gremlin protein levels - not expressed in interdigit region in chicken



(c) Comparison of a chicken foot and a duck foot

a: Courtesy Ed Laufer; b-c: Courtesy of Dr. J.M. Hurle. Originally published in *Development*. 1999 Dec. 126(23):5515–22

- Mutations that changed expression of BMP4 and gremlin provided variation
- In terrestrial settings, **nonwebbed feet** are an advantage
  - ❑Natural selection maintains nonwebbed feet on land
- In aquatic environments, **webbed feet** are an advantage
  - ❑Natural selection would have favored webbed feet
- Speciation may have been promoted by **geographical isolation** of habitats

Hox genes

- Found in all animals
- Variation in the *Hox* genes may have spawned the formation of many **new body plans**
- Number and arrangement of *Hox* genes varies among different types of animals
- Increases in the number of *Hox* genes may have led to greater complexity in body structure

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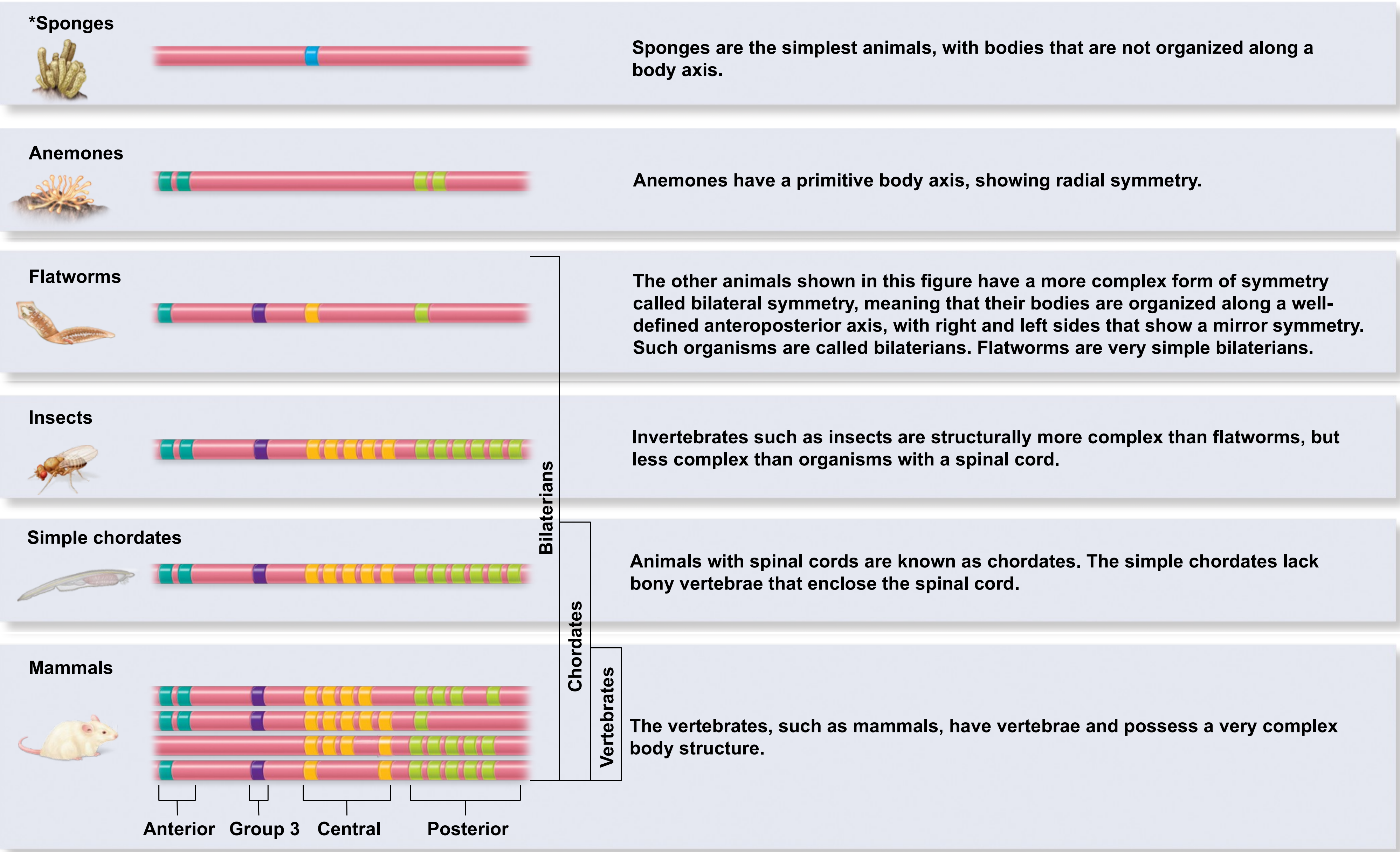


Sponges are the simplest animals, with bodies that are not organized along a body axis.

Anemones have a primitive body axis, showing radial symmetry.

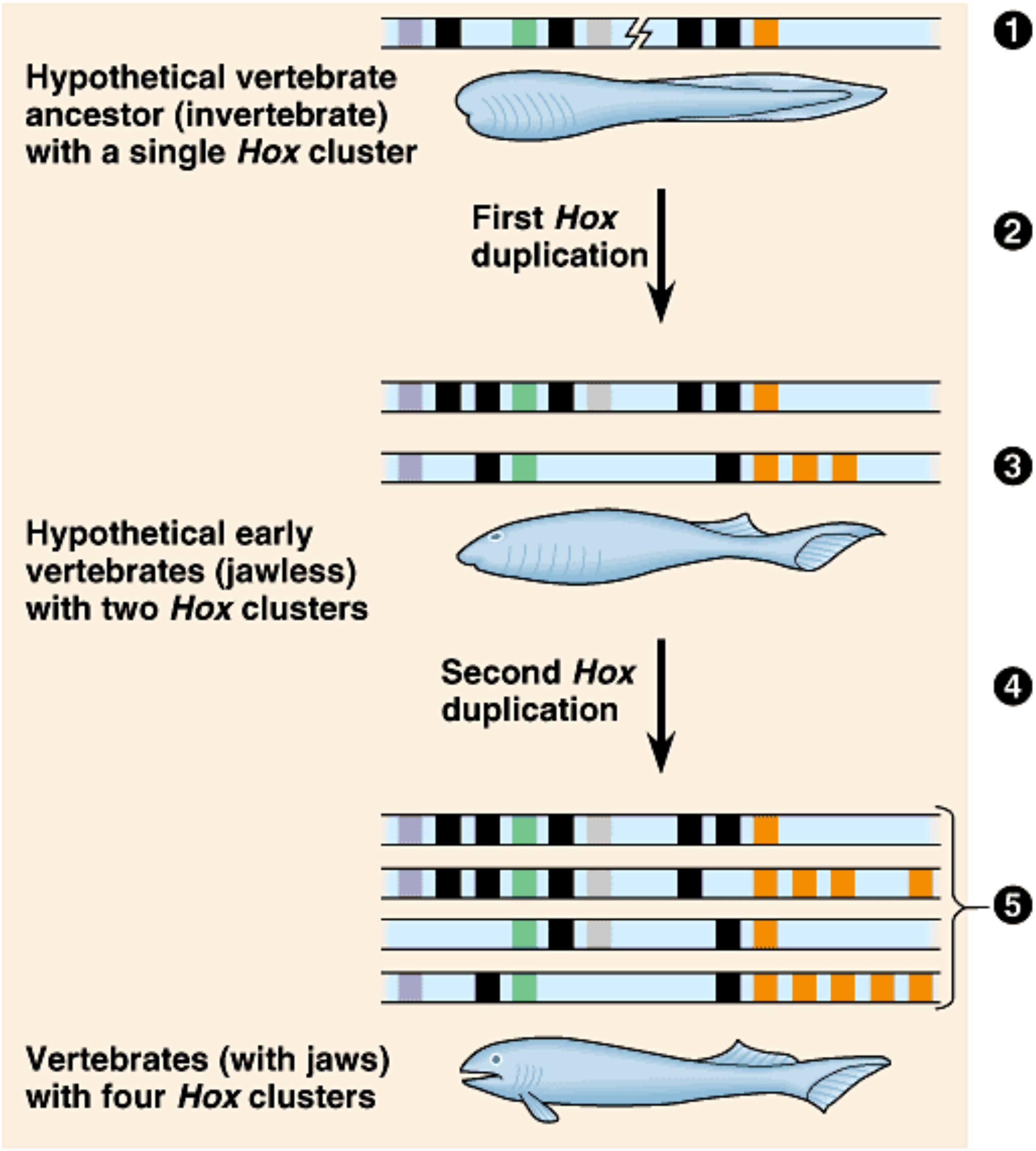
The other animals shown in this figure have a more complex form of symmetry called bilateral symmetry, meaning that their bodies are organized along a well-defined anteroposterior axis, with right and left sides that show a mirror symmetry. Such organisms are called bilaterians. Flatworms are very simple bilaterians.

Invertebrates such as insects are structurally more complex than flatworms, but less complex than organisms with a spinal cord.

Animals with spinal cords are known as chordates. The simple chordates lack bony vertebrae that enclose the spinal cord.

The vertebrates, such as mammals, have vertebrae and possess a very complex body structure.

Hox mutations and the origin of vertebrates



①
Hypothetical vertebrate ancestor (invertebrate) with a single *Hox* cluster
First *Hox* duplication
②
③
Hypothetical early vertebrates (jawless) with two *Hox* clusters
Second *Hox* duplication
④
⑤
Vertebrates (with jaws) with four *Hox* clusters

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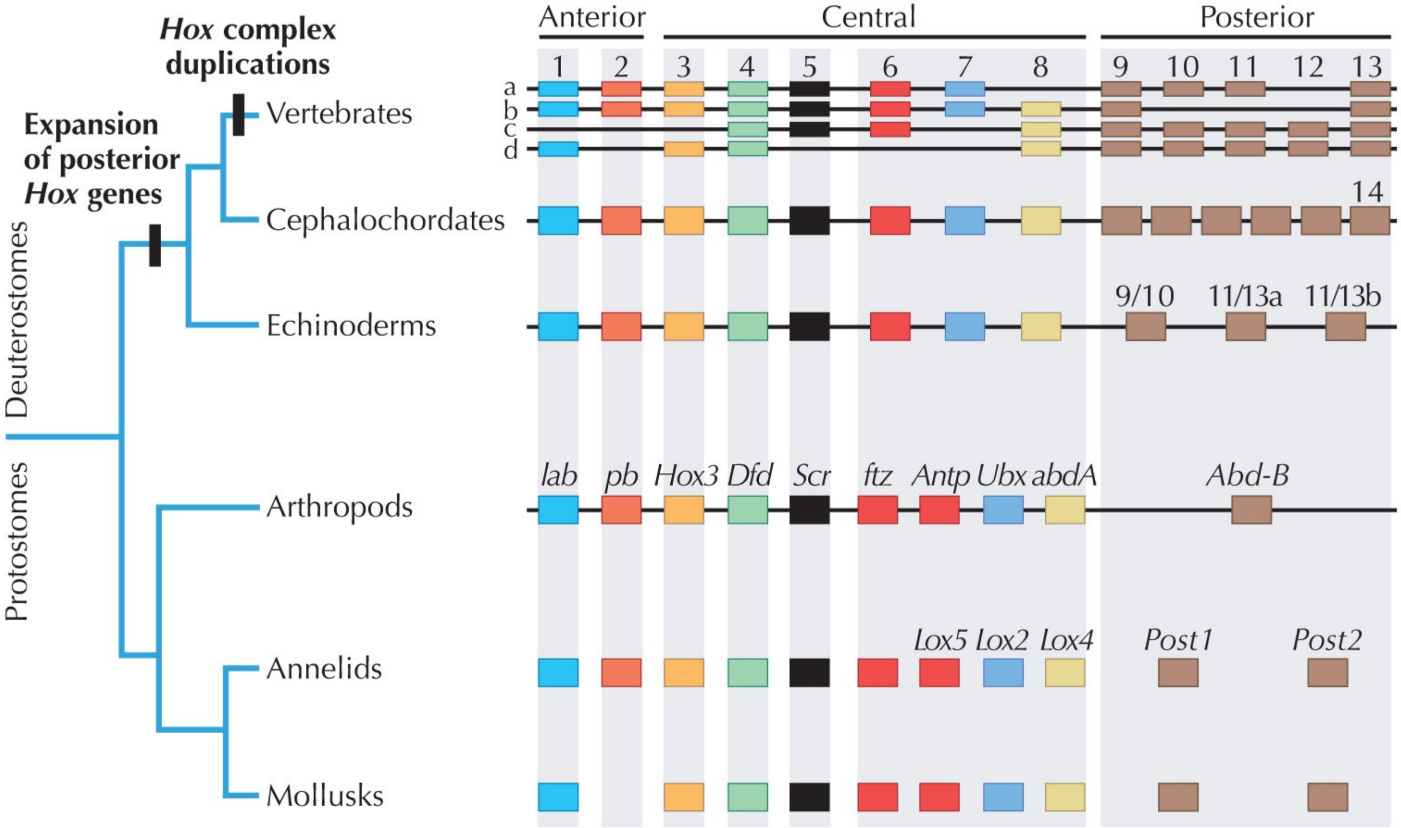
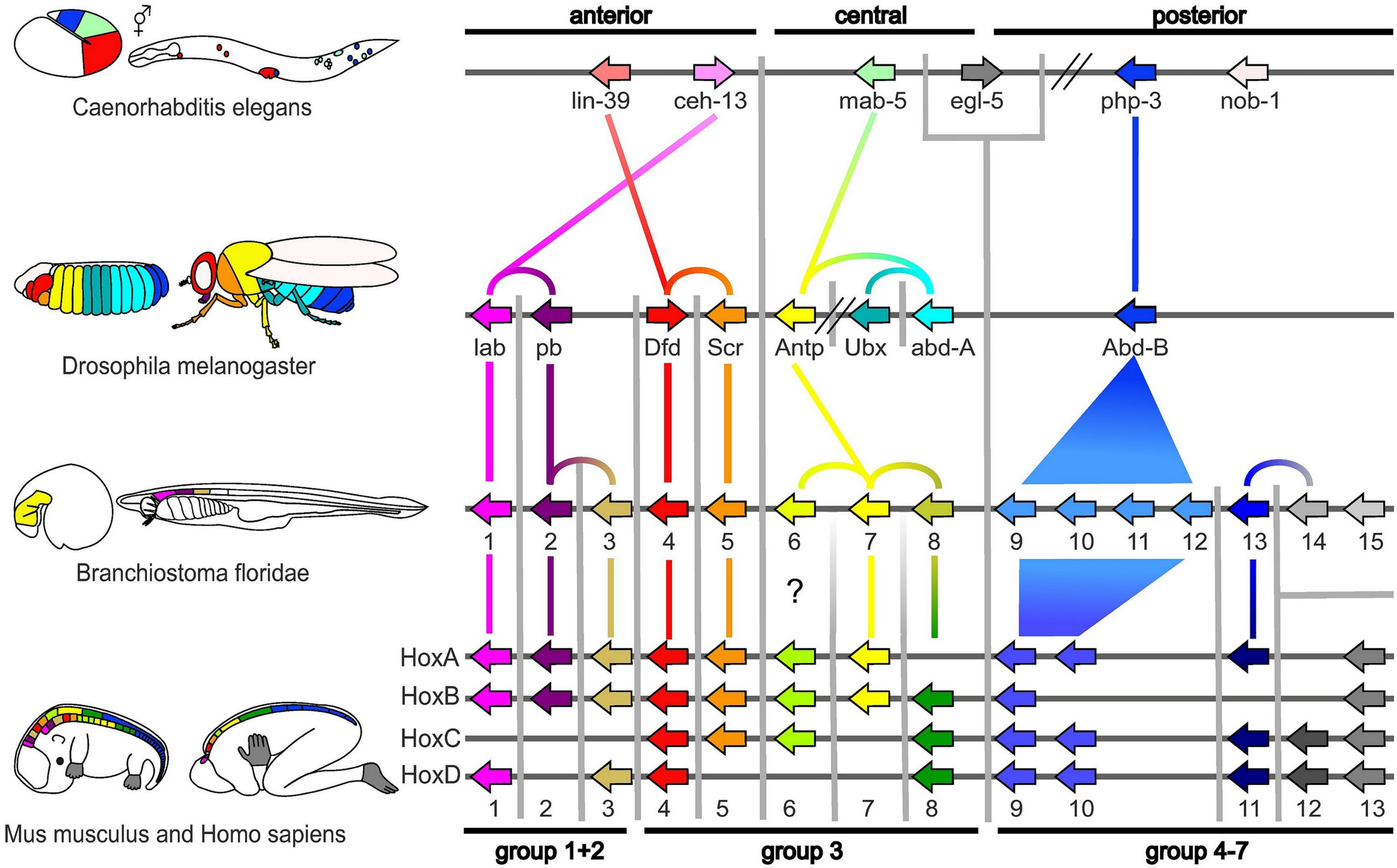


FIGURE 11.6. Evolutionary history of the *Hox* gene complex in metazoan phyla. The common ancestor of the phyla shown here probably possessed at least eight *Hox* genes organized into a single complex. Various expansions of the complex have occurred in multiple lineages. For example, an expansion of the Posterior group appears to have occurred early in deuterostome evolution, and several duplications of the entire cluster occurred during vertebrate evolution, which led to four clusters (a, b, c, and d; note that some *Hox* genes are absent from some of the clusters because of gene loss after duplication) on four different chromosomes. The precise evolutionary relationships for the Posterior class genes and the *Hox6*, *-7*, and *-8* group genes between phyla are still unresolved (e.g., independent duplications may have led to *Hox7* and *-8* in deuterostomes and *Antp* and *Ubx* in protostomes). The coloring pattern shown here for these genes is an oversimplification.

11.6, modified from Carroll S.B. et al., *From DNA to Diversity: Molecular Genetics and the Evolution of Animal Design, 2e*, p. 115, © 2005 Blackwell Publishing

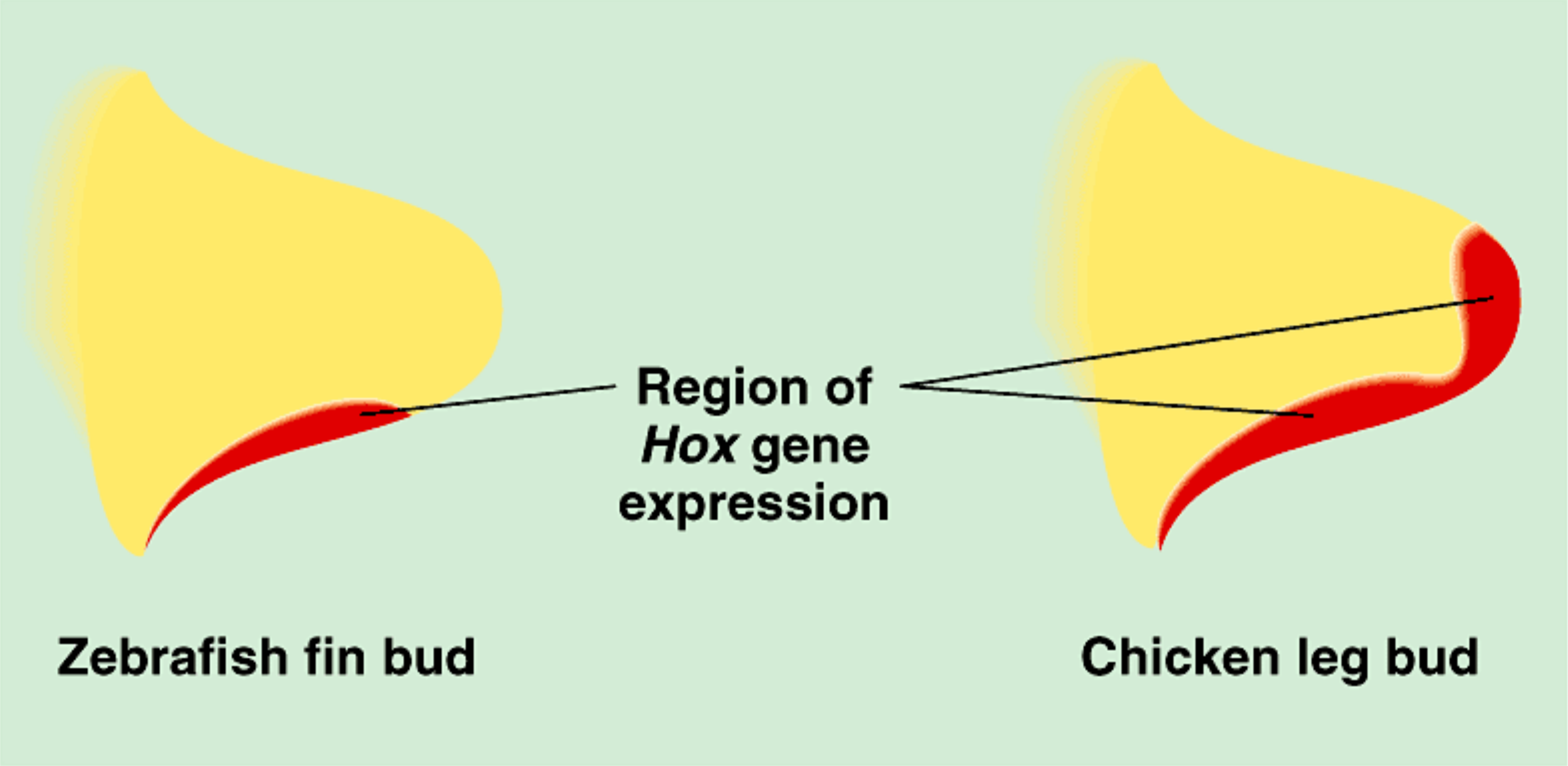
Evolution © 2007 Cold Spring Harbor Laboratory Press



By Stefanie D. Hueber, Georg F. Weiller, Michael A. Djordjevic, Tancred Frickey, CC BY 4.0, https://commons.wikimedia.org/w/index.php?curid=19867115

Human	Chromosome	Genes
HOXA@	chromosome 7	*HOXA1*, *HOXA2*, *HOXA3*, *HOXA4*, *HOXA5*, *HOXA6*, *HOXA7*, *HOXA9*, *HOXA10*, *HOXA11*, *HOXA13*
HOXB@	chromosome 17	*HOXB1*, *HOXB2*, *HOXB3*, *HOXB4*, *HOXB5*, *HOXB6*, *HOXB7*, *HOXB8*, *HOXB9*, *HOXB13*
HOXC@	chromosome 12	*HOXC4*, *HOXC5*, *HOXC6*, *HOXC8*, *HOXC9*, *HOXC10*, *HOXC11*, *HOXC12*, *HOXC13*
HOXD@	chromosome 2	*HOXD1*, *HOXD3*, *HOXD4*, *HOXD8*, *HOXD9*, *HOXD10*, *HOXD11*, *HOXD12*, *HOXD13*

Hox genes and the evolution of tetrapod limbs



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- *Hox* gene complexity has been instrumental in the evolution and speciation of animals with different body patterns
- Three lines of evidence support this idea:
  - *Hox* genes are known to **control fate** of regions along the antero-posterior axis
  - General trend for more complex animals to have **more *Hox* genes** and *Hox* clusters
  - Comparison of *Hox* gene evolution and animal evolution bear **striking parallels**

Developmental genes that affect growth rate

- Genetic variation can influence morphology by controlling relative **growth rates** of different parts of the body during development
- **Heterochrony** – evolutionary changes in the rate or timing of developmental events
- Compare head growth between human and chimpanzee
- **Paedomorphosis** – sexually mature organism may retain traits typical of the juvenile stage of the organism’s ancestor

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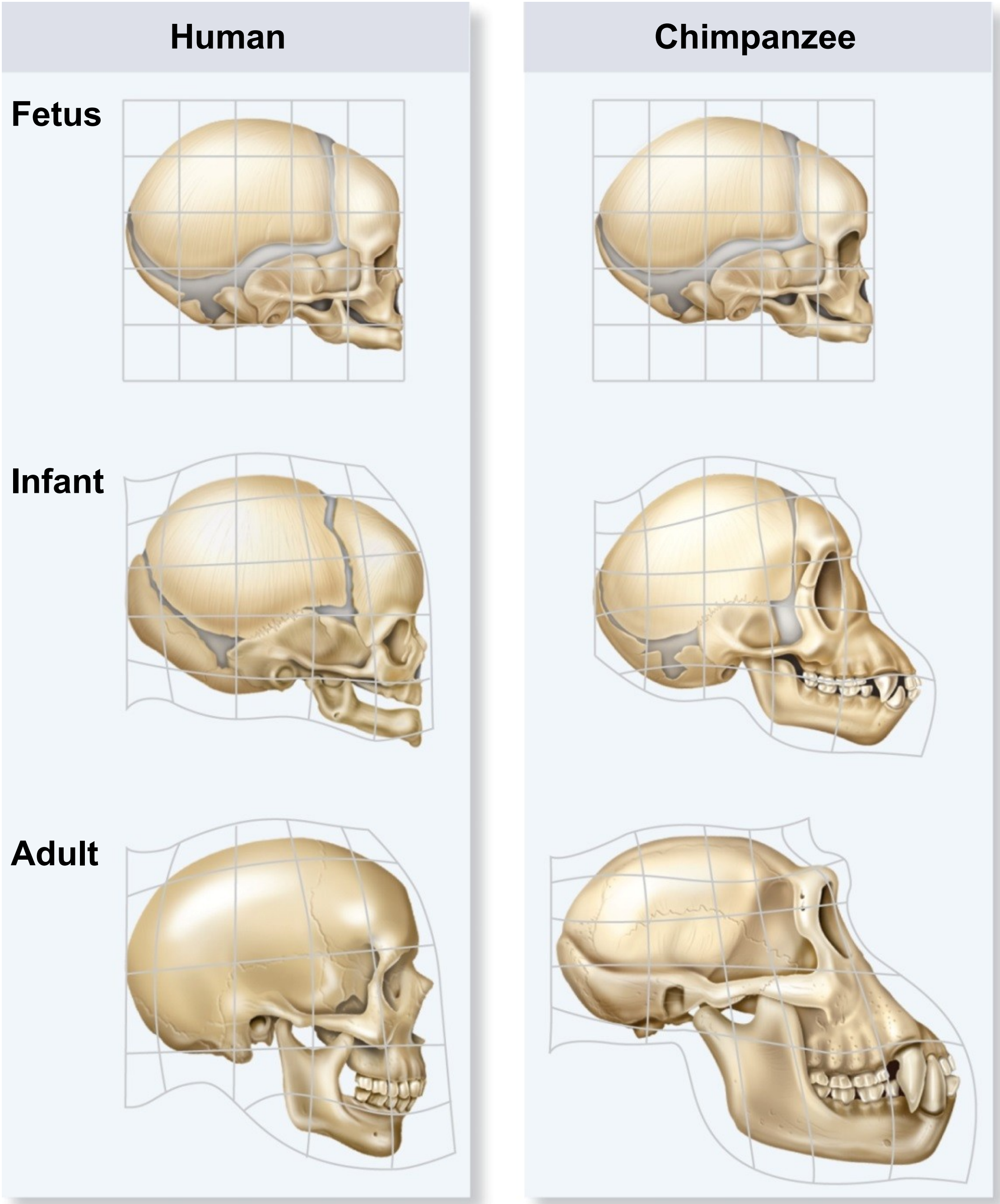
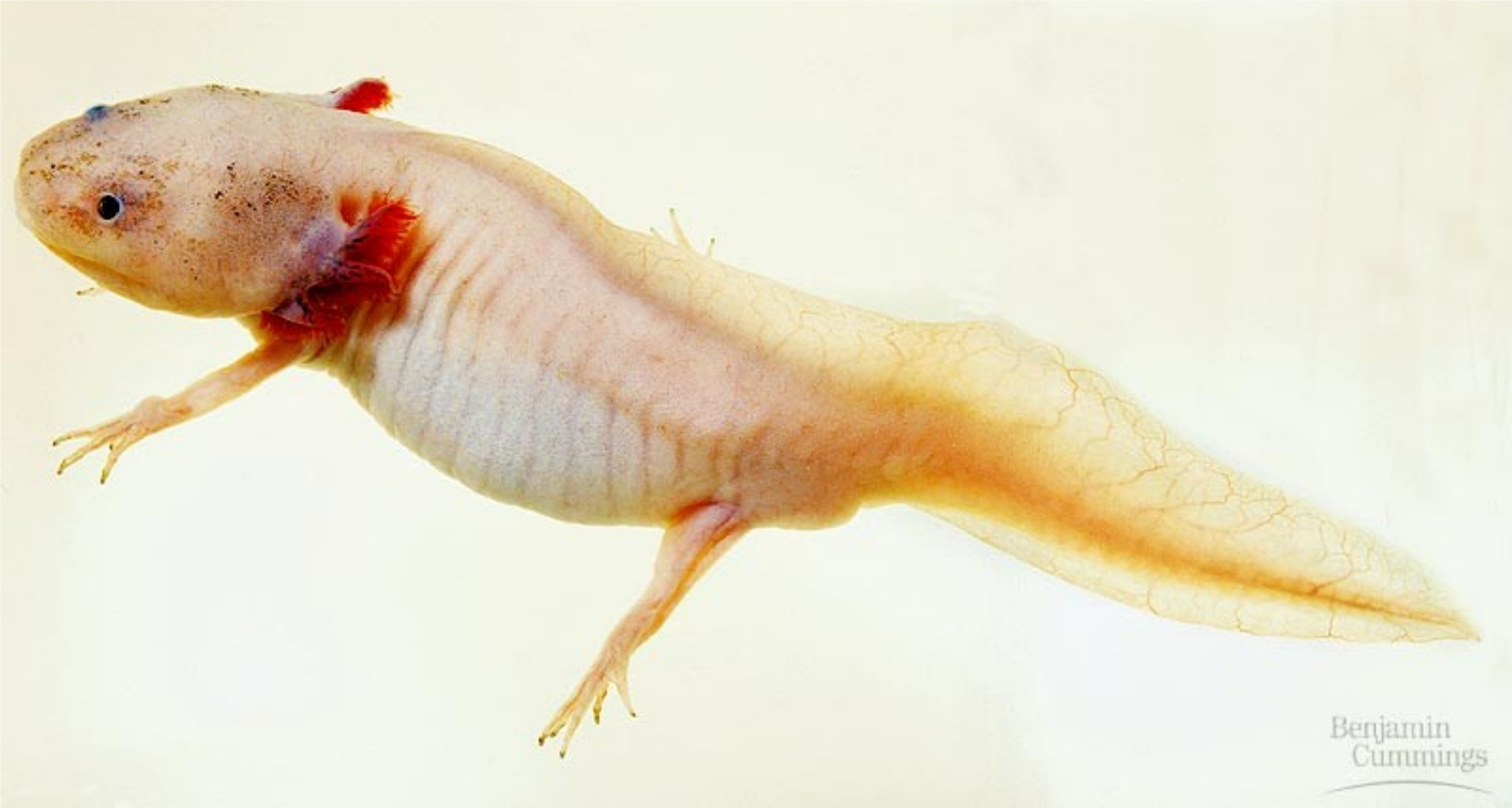


Paedomorphosis



The Study of the *Pax6* Gene Indicates That Different Types of Eyes Evolved from a Simpler Form

- Explaining how a complex organ comes into existence is a major challenge
- Researchers have discovered many different types of eyes
- Thought that eyes may have independently arisen many different times during evolution
- *Pax6* is a **master control gene** that controls the expression of many other genes and influences eye development

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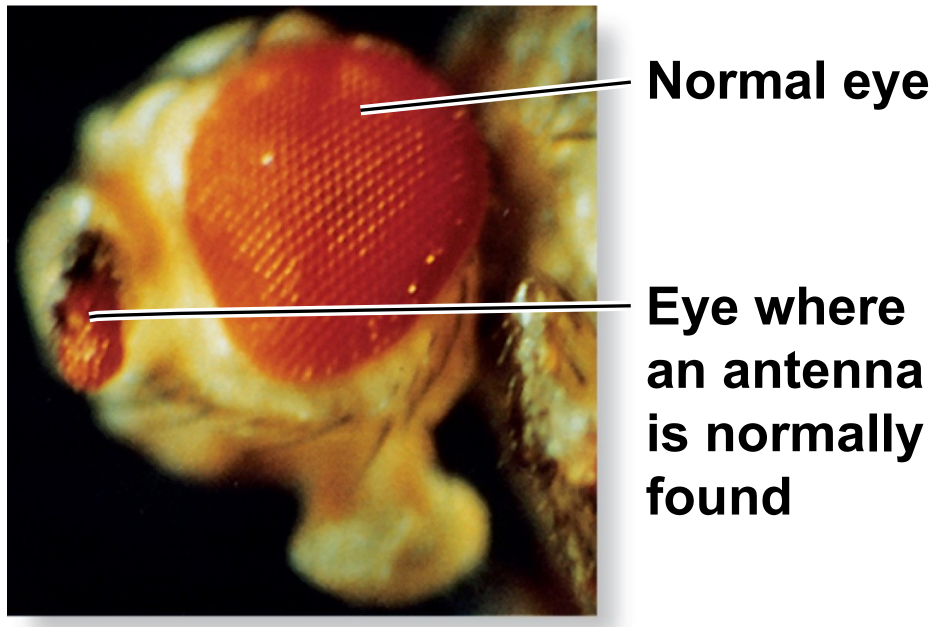
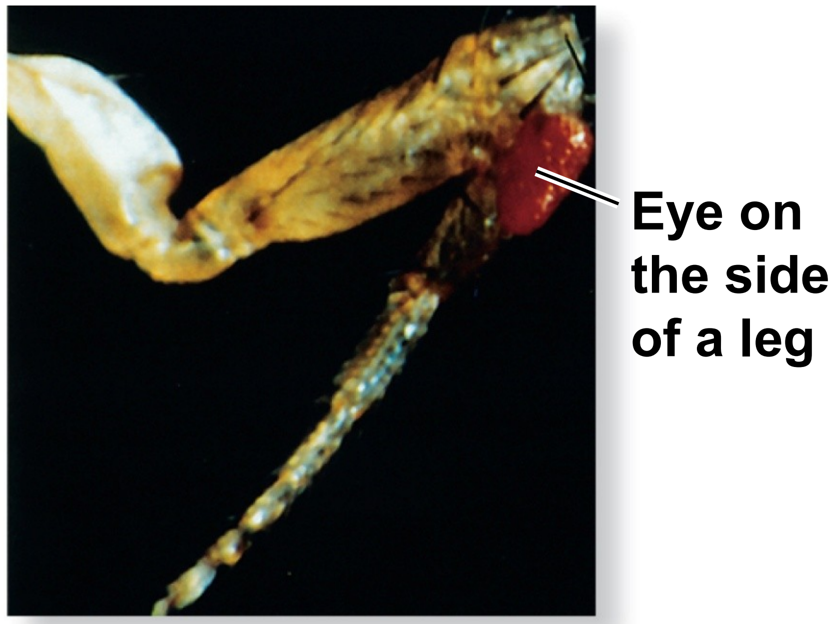


(a) Abnormal expression of the *Drosophila eyeless* gene in the antenna region



(b) Abnormal expression of the mouse *Pax6* gene in a fruit fly leg

a-b: © Prof. Walter J. Gehring, University of Basel

- Eyes of *Drosophila* and mammals are evolutionarily derived from a modification of a very simple eye that **arose once during evolution**
- If *Drosophila* and mammalian eyes had arisen independently, the *Pax6* gene from mice would not be expected to induce the formation of eyes in *Drosophila*
- Hypothesized that the eyes from many different species all evolved from a common ancestral form consisting of, as proposed by Darwin, **one photoreceptor cell and one pigment cell**

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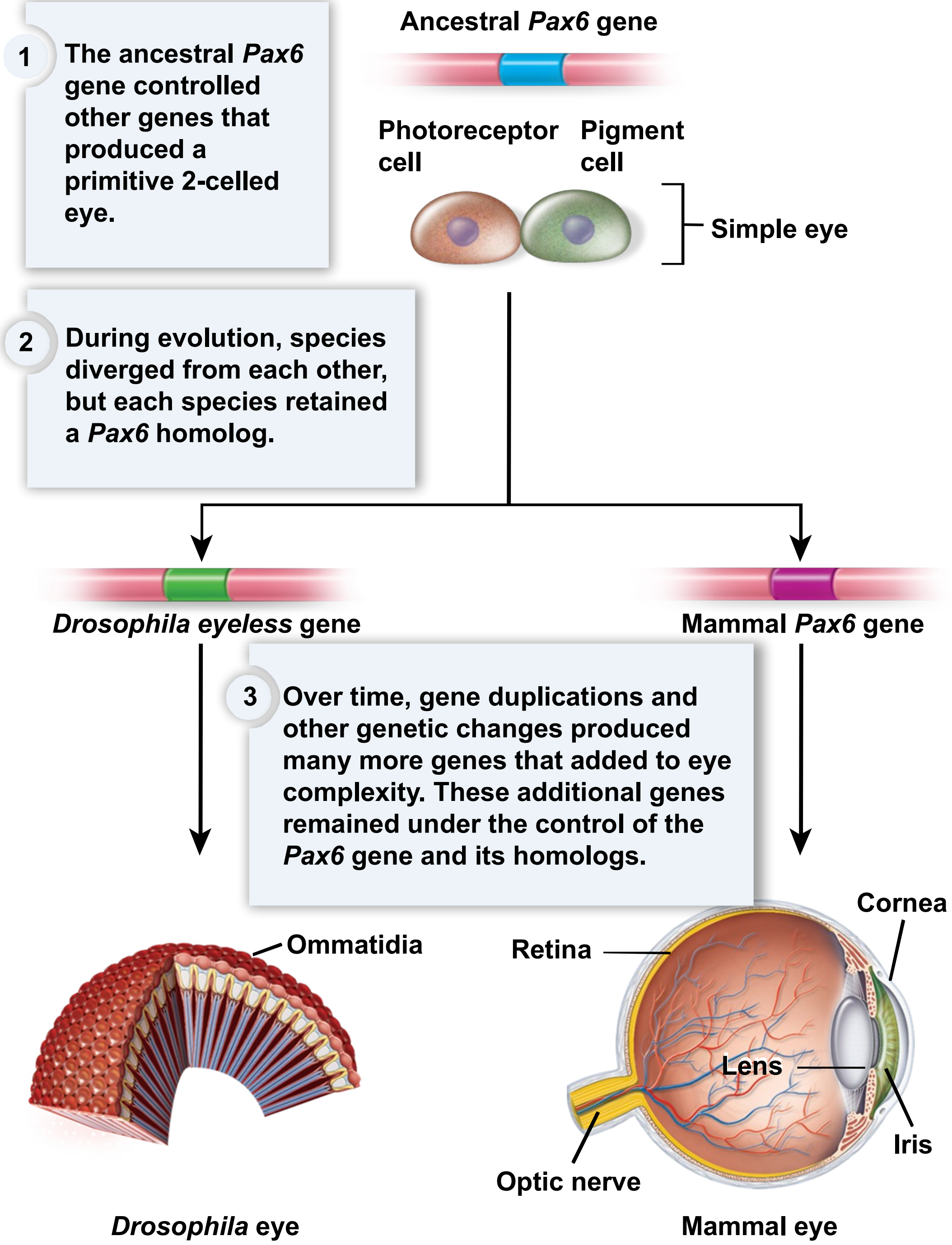


1 The ancestral *Pax6* gene controlled other genes that produced a primitive 2-celled eye.

2 During evolution, species diverged from each other, but each species retained a *Pax6* homolog.

3 Over time, gene duplications and other genetic changes produced many more genes that added to eye complexity. These additional genes remained under the control of the *Pax6* gene and its homologs.

Crash Course Evo Devo

Population Evolution and Genetics

Key Concepts:

- **Genes in Populations**
- **Natural Selection**
- **Sexual Selection**
- **Genetic Drift**
- **Migration and Nonrandom Mating**

The Modern Synthesis

- An integration of Darwinian natural selection and population genetics
- Formulated in the first half of the 20th century
- How do evolutionary processes like natural selection affect the genetic makeup of a population?
- How does this result in gradual evolution of populations and species?
- This theory connects microevolution with macroevolution.

Microevolution

- Defined: Changes in the frequency of alleles in a population's gene pool from generation to generation
- Change because of:
  - ❑Introduction of **new genetic variation** (mutations, gene duplication, exon shuffling, horizontal gene transfer)
    - Not a major factor dictating allele frequencies
  - ❑**Evolutionary mechanisms** that alter the prevalence of an allele or genotype (natural selection, random genetic drift, migration, nonrandom mating)
    - Potential for widespread genetic change

Macroevolution

- Evolutionary processes that give rise to new species and higher taxonomic groups (genera, families, classes, etc.)
- Speciation
- Evolution of antibiotic resistance in bacteria, if it leads to new species of bacteria.
- Viral evolution - new virus strains (even though viruses are not living). (Flu shots every year)

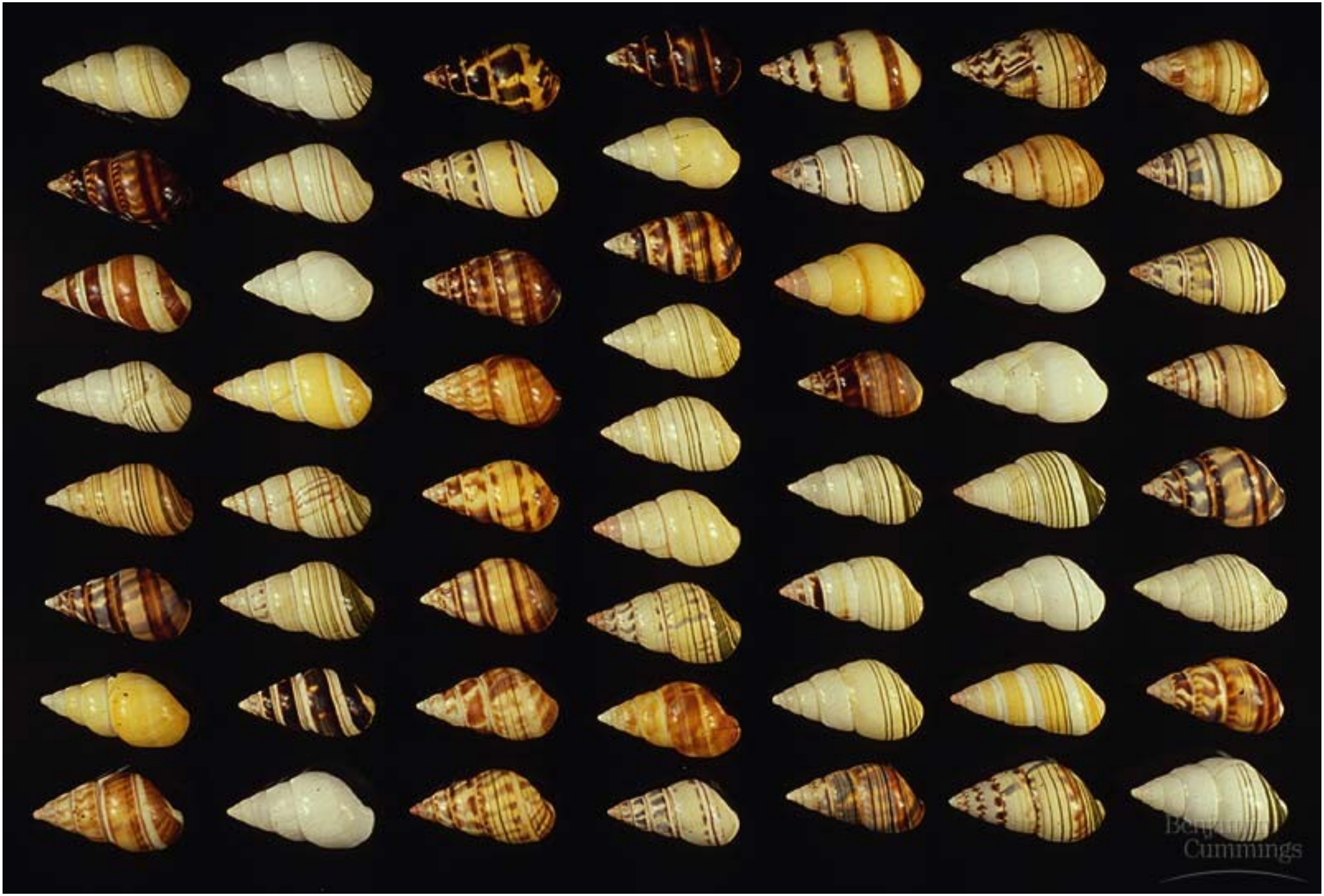
Genes in Populations

- **Population Genetics** – Study of genes and genotypes within and between populations
- How do genes (alleles) vary over time?
- How is genetic variation related to phenotypic variation?
- Allele frequencies versus genotype frequencies.

Evolution in Populations

- **Population genetics** – study of the genetic variation within and between populations
- Population – localized group of individuals of the **same species**
- **Individual organisms do NOT evolve: populations DO**
- **Gene Pool** – total of all alleles (genes) within a population
- **Gene Flow** – movement of alleles within and between populations

Shells: all the same species (*Liguus fascitus*)



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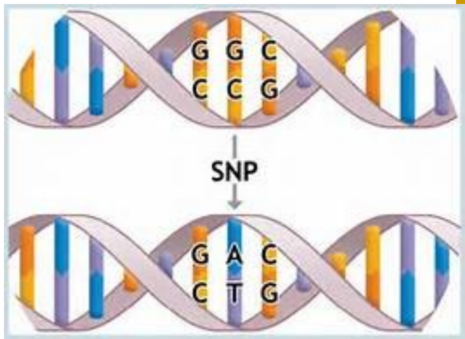
Genes Are Usually Polymorphic

- Polymorphism – traits display variation within a population
  - Due to two or more alleles that influence phenotype
- **Polymorphic gene** – two or more alleles
- **Monomorphic gene** – predominantly single allele
- **Single nucleotide polymorphisms (SNPs)**
  - Smallest type of genetic change in a gene
  - Most common – 90% of variation in human gene sequences
- Large, healthy populations exhibit a high level of genetic diversity
- Raw material for evolution



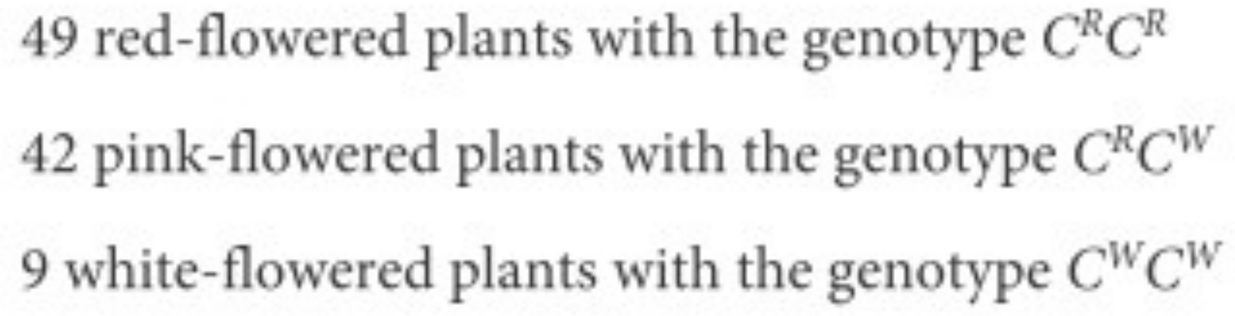
Allele and genotype frequencies

- Related but distinct calculations
- Think of frequency as a **percentage**

$$\text{Allele frequency} = \frac{\text{Number of copies of a specific allele in a population}}{\text{Total number of all alleles for that gene in a population}}$$

$$\text{Genotype frequency} = \frac{\text{Number of individuals with a particular genotype in a population}}{\text{Total number of individuals in a population}}$$

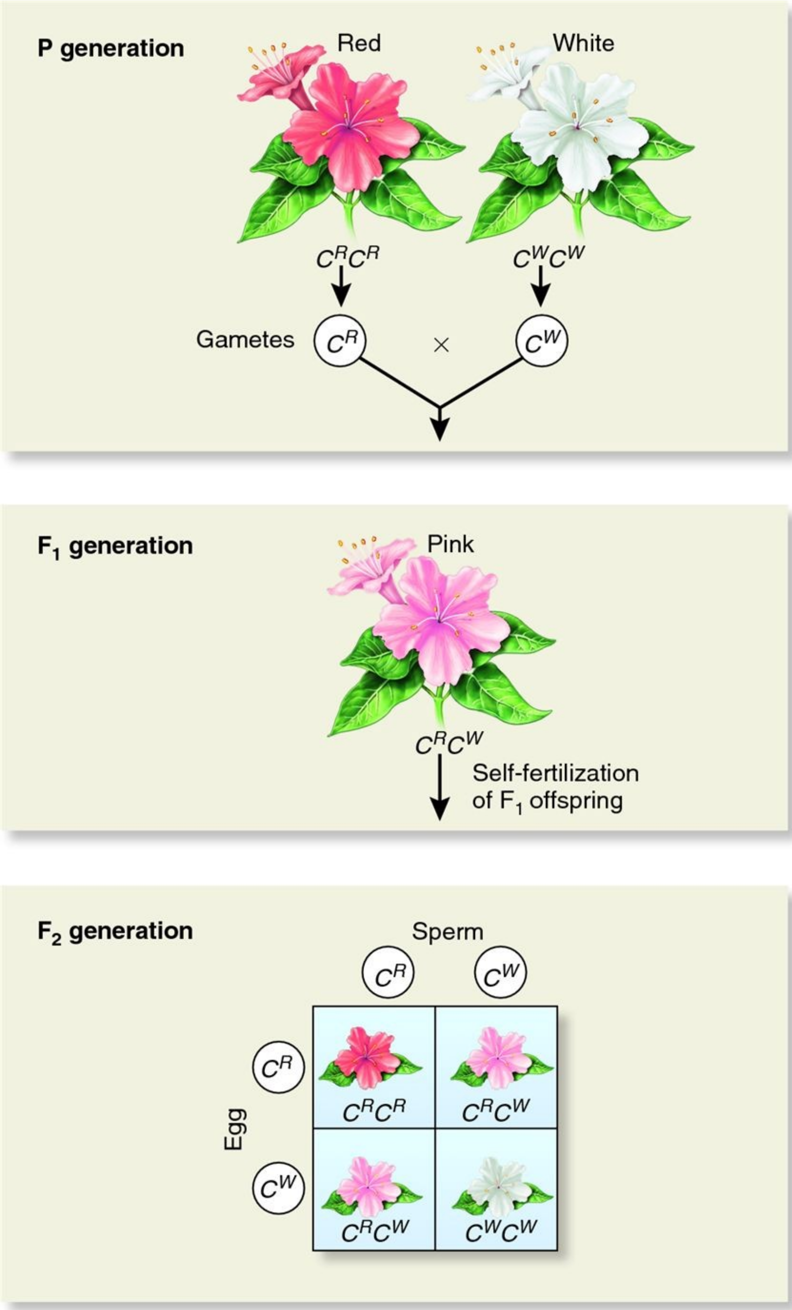
Example: Four o’clock plants



49 red-flowered plants with the genotype C^RC^R

42 pink-flowered plants with the genotype C^RC^W

9 white-flowered plants with the genotype C^WC^W



Statement of Hardy-Weinberg

BI-ALLELIC SYSTEM

- p = frequency of one allele in the population (say C^R)

Statement of Hardy-Weinberg

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- **p = frequency of one allele in the population (say C^R)**
- **q = frequency of the other allele (C^w)**

Statement of Hardy-Weinberg

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- p = frequency of one allele in the population (say C^R)
- q = frequency of the other allele (C^w)
- p + q = 1 (%p + %q = 100%)

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- p^2 = frequency of C^RC^R genotype (homozygous dominant)

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- p^2 = frequency of C^RC^R genotype (homozygous dominant)
- q^2 = frequency of C^WC^W genotype (homozygous recessive)
- $2pq$ = frequency of C^RC^W genotype (heterozygote)

Hardy-Weinberg equation

$$p^2 + 2pq + q^2 = 1$$

p^2 = the genotype frequency of $C^R C^R$ homozygotes **Red homozygotes**

$2pq$ = the genotype frequency of $C^R C^W$ heterozygotes **Pink heterozygotes**

q^2 = the genotype frequency of $C^W C^W$ homozygotes **White homozygotes**

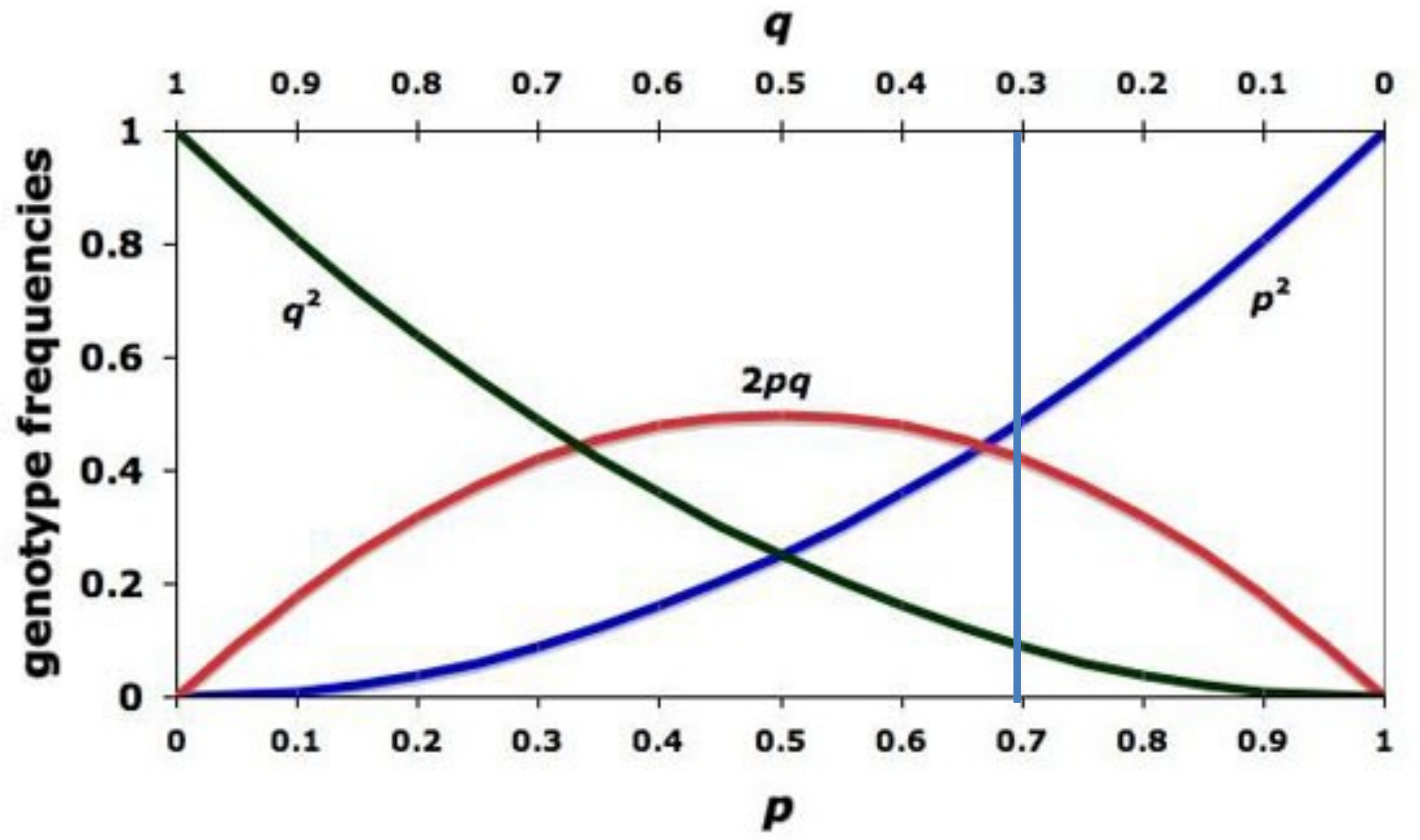
If $p = 0.7$ and $q = 0.3$, then

Frequency of $C^R C^R = p^2 = (0.7)^2 = 0.49$

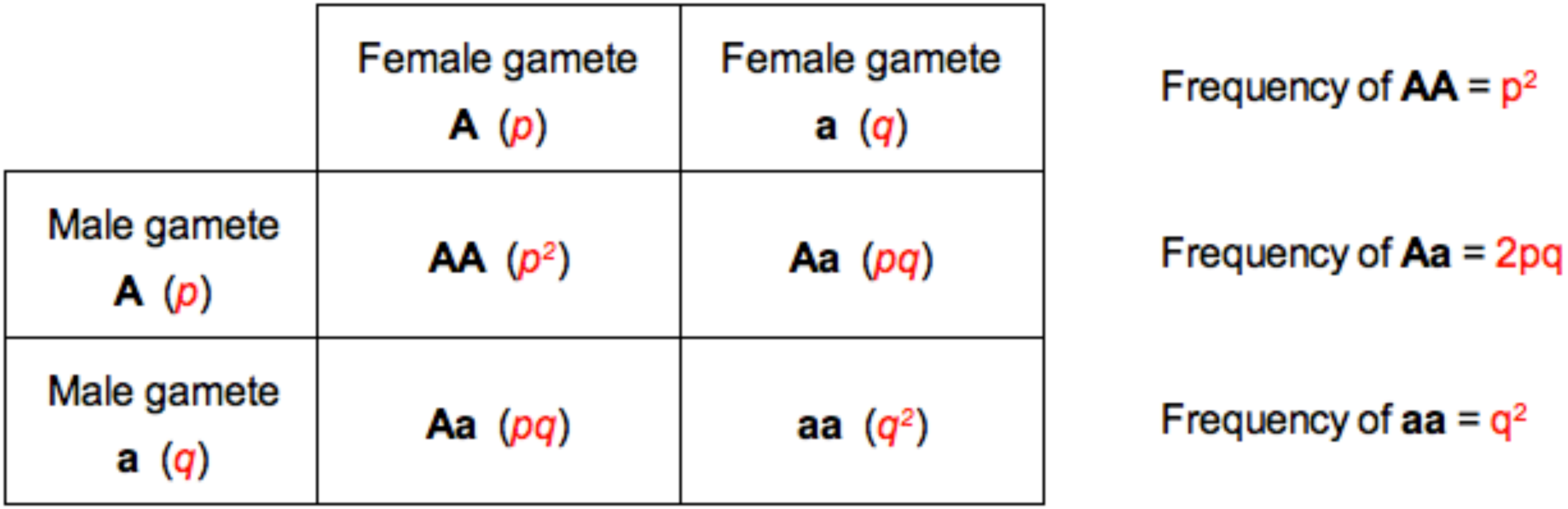
Frequency of $C^R C^W = 2pq = 2(0.7)(0.3) = 0.42$

Frequency of $C^W C^W = q^2 = (0.3)^2 = 0.09$

Hardy Weinberg allele and genotype frequencies



Derivation of equation

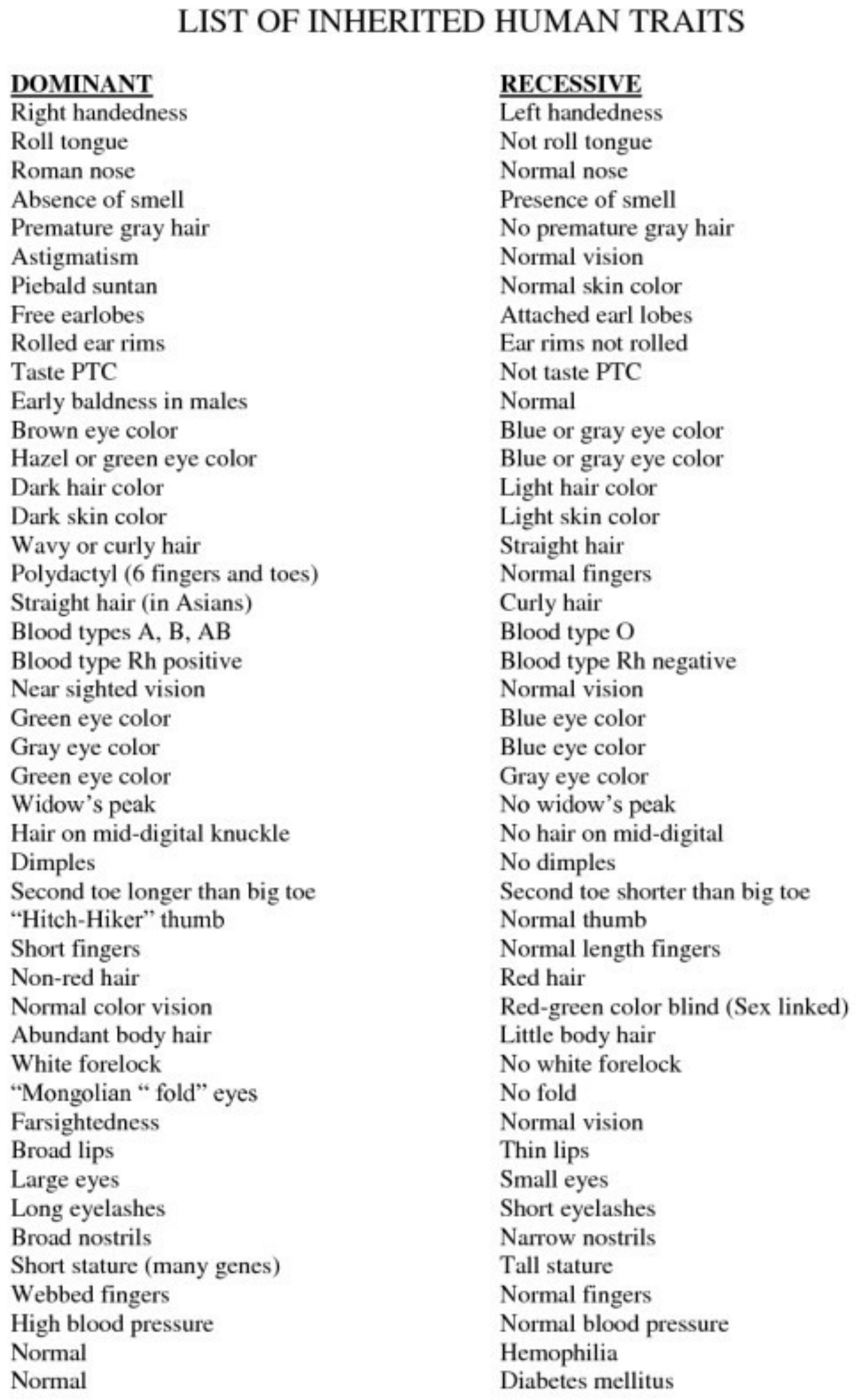


	Female gamete **A** (p)	Female gamete **a** (q)
Male gamete **A** (p)	**AA** (p^2)	**Aa** (pq)
Male gamete **a** (q)	**Aa** (pq)	**aa** (q^2)

Frequency of **AA** = p^2

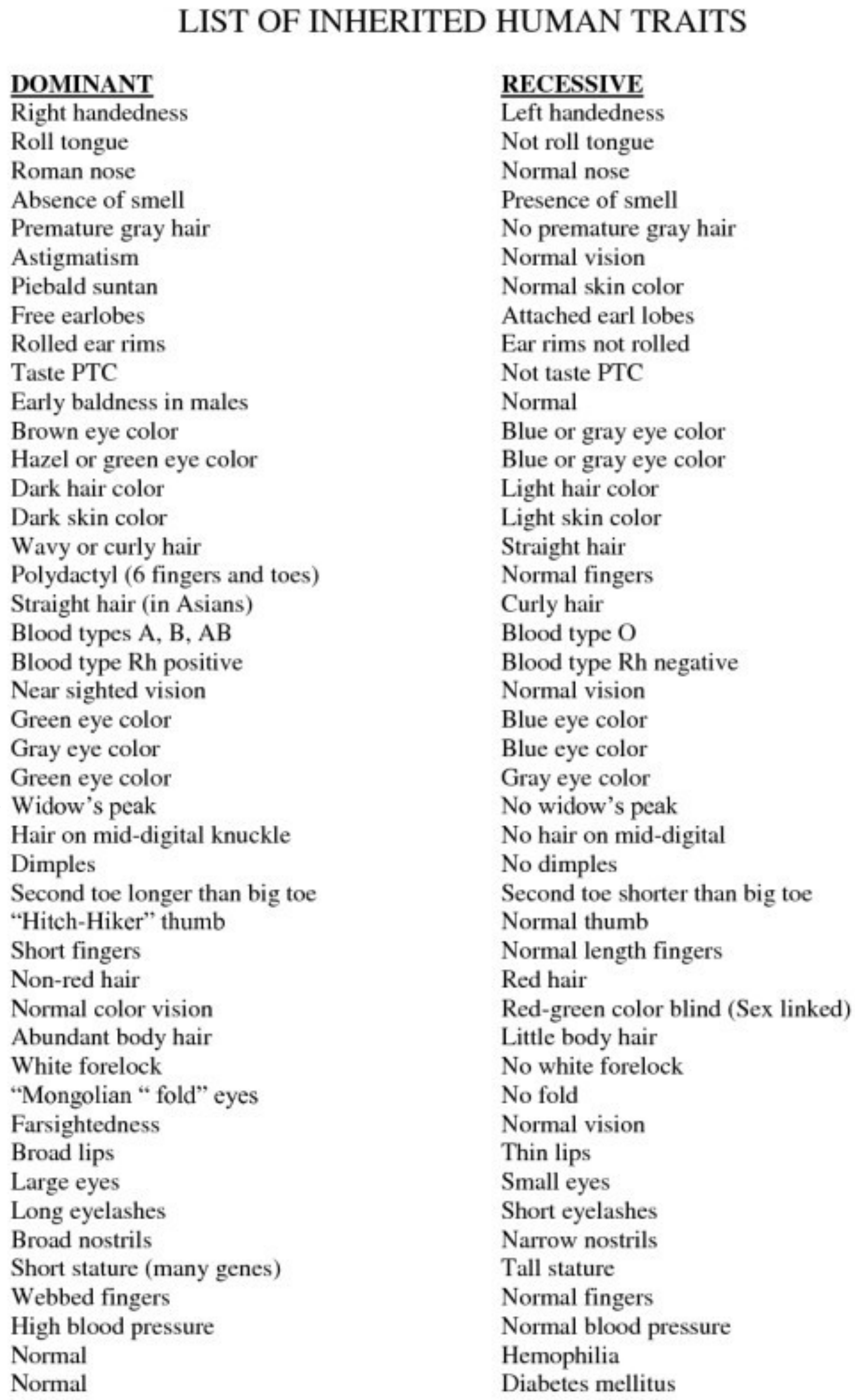
Frequency of **Aa** = $2pq$

Frequency of **aa** = q^2



LIST OF INHERITED HUMAN TRAITS

DOMINANT	**RECESSIVE**
Right handedness	Left handedness
Roll tongue	Not roll tongue
Roman nose	Normal nose
Absence of smell	Presence of smell
Premature gray hair	No premature gray hair
Astigmatism	Normal vision
Piebald suntan	Normal skin color
Free earlobes	Attached earl lobes
Rolled ear rims	Ear rims not rolled
Taste PTC	Not taste PTC
Early baldness in males	Normal
Brown eye color	Blue or gray eye color
Hazel or green eye color	Blue or gray eye color
Dark hair color	Light hair color
Dark skin color	Light skin color
Wavy or curly hair	Straight hair
Polydactyl (6 fingers and toes)	Normal fingers
Straight hair (in Asians)	Curly hair
Blood types A, B, AB	Blood type O
Blood type Rh positive	Blood type Rh negative
Near sighted vision	Normal vision
Green eye color	Blue eye color
Gray eye color	Blue eye color
Green eye color	Gray eye color
Widow's peak	No widow's peak
Hair on mid-digital knuckle	No hair on mid-digital
Dimples	No dimples
Second toe longer than big toe	Second toe shorter than big toe
"Hitch-Hiker" thumb	Normal thumb
Short fingers	Normal length fingers
Non-red hair	Red hair
Normal color vision	Red-green color blind (Sex linked)
Abundant body hair	Little body hair
White forelock	No white forelock
"Mongolian " fold" eyes	No fold
Farsightedness	Normal vision
Broad lips	Thin lips
Large eyes	Small eyes
Long eyelashes	Short eyelashes
Broad nostrils	Narrow nostrils
Short stature (many genes)	Tall stature
Webbed fingers	Normal fingers
High blood pressure	Normal blood pressure
Normal	Hemophilia
Normal	Diabetes mellitus



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Normal	Hemophilia
Normal	Diabetes mellitus

Widow's peak

- This is a dominant trait.

Widow’s peak (dominant)
Zoom poll

- How many # students in the class? 103
- How many student’s do NOT have widow’s peak? 78.

Frequency or proportion of this recessive genotype (q^2)?

Widow’s peak (dominant)
Zoom poll

- How many # students in the class?
- How many student’s do NOT have widow’s peak?
- Minus widow’s peak is the recessive trait, so what is their genotype? We will use W=widow’s peak allele and w =no widow’s peak allele.
- What is the **genotype** frequency of ww?
- If p=frequency of W, and q =frequency of w, how can you calculate the frequency of q? **-->**

Widow’s peak (dominant)
Zoom poll

- How many # students in the class? 103
- How many student’s do NOT have widow’s peak? 78.

Genotype frequency (ww) = 78/103 =0.76

Widow’s peak (dominant)
Zoom poll

- How many # students in the class? 103
- How many student’s do NOT have widow’s peak? 78.

Genotype frequency (ww) = 78/103 =0.76 (76%)=q^2

So, what is the allele frequency of q?

Widow’s peak (dominant) Zoom poll

- How many # students in the class? 103
- How many student’s do NOT have widow’s peak? 78.

Genotype frequency (ww) = 78/103 =0.76 (76%)=q^2

So, what is the allele frequency of q?

Square root of 0.76 = square root of q^2 = 0.87

Widow’s peak
# total, # yes, # no

- What did you calculate for q?
    - How did you get this?
- What did you calculate for p? 1-0.87=0.13
    - How did you get this?
- How do you solve for genotype frequencies?
- Start with genotype frequency for homozogous recessives in class (those without widow’s peak)

Widow's Peak

- Allele frequencies q=0.87 p=0.13
  - p + q = 1 (p and q are percentages in decimal form) { %p + %q = 100%}
- Genotype frequencies
  - $P^2 + 2pq + q^2 = 1$ { $\%p^2 + \%2pq + \%q^2 = 100\%$}
    - P^2 = frequency of homozygous dominants 0.04
    - **q^2** = frequency of homozygous **recessives 0.76**
      2pq = frequency of heterozygotes = 0.32
    - Check your work: Do they add up to 1?

Review for class data

- 103 students, 78 non-widow's peak
- 78/103=0.76 genotype frequency for homozygous recessive
- sq. rt of 0.76=0.87 = q allele frequency for recessive allele
- p+q=1, so 1-.87=.13 = p or allele frequency of dominant allele
- 0.017+0.226+0.76

Hardy Weinberg Equation of Population Genetics

ASSUMPTIONS

1. Large population - to ensure no sampling error from one generation to the next
2. Random mating - no assortative mating or mating by genotype
3. No mutations
4. No migration between populations
5. No selection - all genotypes reproduce with equal success

STATES: If all of the above, ALLELE frequency WILL NOT CHANGE from generation to generation

Example Problem

- **If 9% of an African population is born with a severe form of sickle-cell anemia (ss), what percentage of the population will be more resistant to malaria because they are heterozygous(Ss) for the sickle-cell gene?**

Calculating the heterozygote genotype frequency

- 0.09=s^2 =homozygous recessive genotype frequency
- 9% = 0.09

$P^2 + 2pq + q^2 = 1$, $p + q = 1$

- 0.09=s^2 =homozygous recessive genotype frequency
- s =0.3 = square root of 0.09 = allele frequency of s

$P^2 + 2pq + q^2 = 1, \quad p + q = 1$

- $0.09 = s^2$ = homozygous recessive genotype frequency
- $s = 0.3$ = square root of 0.09 = allele frequency of s
- $s + \underline{S} = 1$, so $\underline{S} = 0.7$ = allele frequency of $\underline{S}$

$P^2 + 2pq + q^2 = 1, \quad p + q = 1$

- $0.09 = s^2$ =homozygous recessive genotype frequency
- $s = 0.3$ = square root of 0.09 = allele frequency of s
- $s + \underline{S} = 1$, so $\underline{S} = 0.7$ = allele frequency of $\underline{S}$
- What is S^2 ? 0.49 = homozygous dominant gen. freq.

$P^2 + 2pq + q^2 = 1, \quad p + q = 1$

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- What is S^2 ? 0.49 = homozygous dominant gen. freq.
- What is the heterozygote genotype frequency ?
- $\underline{S}^2 + 2\underline{S}s + s^2 = 1$ $\qquad$ $0.49 + 2\underline{S}s + 0.09 = 1$

$P^2 + 2pq + q^2 = 1$, $p + q = 1$

- $0.09 = s^2$ =homozygous recessive genotype frequency
- s =0.3 = square root of 0.09 = allele frequency of s
- s + S = 1, so S = 0.7 = allele frequency of S
- What is S^2 ? 0.49 = homozygous dominant gen. freq.
- What is the heterozygote genotype frequency ?
- $\underline{S}^2 + 2\underline{S}s + s^2 = 1$ $0.49 + 2\underline{S}s + 0.09 = 1$
- 0.42

$P^2 + 2pq + q^2 = 1$, $p + q = 1$

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- What is the heterozygote genotype frequency ?
- $\underline{S}^2 + 2\underline{S}s + s^2 = 1$ $0.49 + 2\underline{S}s + 0.09 = 1$
- 0.42
- 49% homo dominant, 9% homo recessive, 42% heterozygotes

- Suppose we had a population of 500 individuals, in which 36% of individuals were albino (albinism is a recessive characteristic = aa)
- Using the equations: $p + q = 1$ **and** $p^2 + 2pq + q^2 = 1$
- ● If $q^2 = 0.36$ ð $q = 0.6$ ($\sqrt{0.36}$)
- ● If $q = 0.6$ ð $p = 0.4$ ($p + 0.6 = 1$)
- ● If $p = 0.4$ ð $p^2 = 0.16$ (0.4×0.4)
- ● Therefore $2pq = 0.48$ ($2 \times 0.4 \times 0.6$)

Natural Selection

- Phenotypic traits that are heritable, and give a survival or reproductive advantage to an individual, become more common in successive generations (think Galapagos finches)
- Over time, natural selection results in **adaptations -** changes in phenotypes and their underlying genotypes in populations of living organisms that promote their survival and reproduction in a particular environment

Natural selection does not act on individual alleles, however, but on entire organisms – the whole phenotype.

Populations evolve, not individuals. Microevolution is measured in the population. But, natural selection acts on individuals, not populations.

- **Reproductive success (fitness)**
  - Likelihood of an individual contributing fertile offspring to the next generation
  - Relative likelihood that a genotype will contribute to the gene pool of the next generation as compared to other genotypes

FITNESS

- Attributed to two categories of traits
  - Certain characteristics make organisms better adapted and more likely to **survive** to reproductive age
  - Traits may be directly associated with **reproduction**, such as ability to find a mate and ability to produce viable gametes and offspring

Cardinals

Modern description of natural selection (Darwin’s postulates re-stated)

1. Within a population, allelic variation arises from random mutations that cause differences in DNA sequences
2. The products of some alleles enhance an individual’s survival or reproductive capability compared to other members of the population
3. Individuals with advantageous alleles are more likely to survive and contribute their alleles to the gene pool of the next generation
4. Over the course of many generations, allele frequencies of many different genes may change through natural selection, thereby significantly altering the characteristics of a population

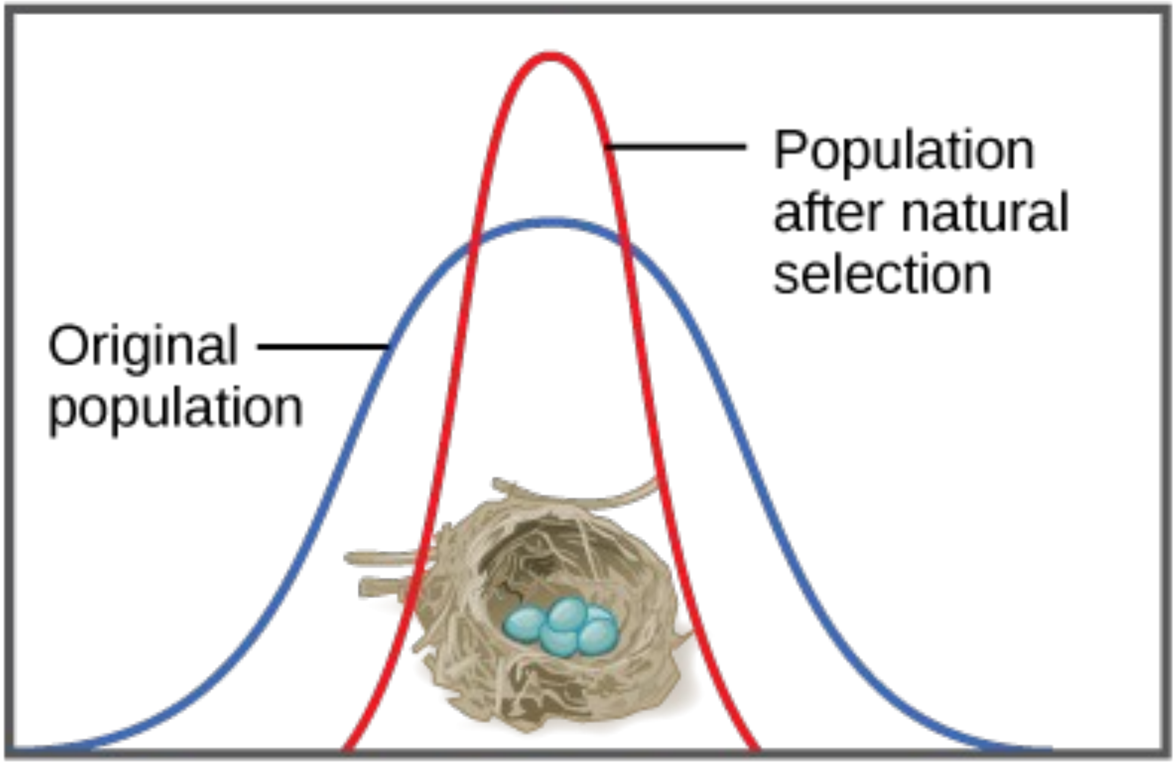
Natural selection patterns – how does selection proceed?

- Stabilizing selection
- Directional selection
- Disruptive/Diversifying selection
- Frequency-dependent
- Balancing selection
- Sexual selection

Stabilizing selection

- Favors the survival of individuals with intermediate phenotypes
- Extreme values of a trait are selected against
- Clutch size
  - ❑Too many eggs and offspring – die due to lack of care and food
  - ❑Too few eggs – does not contribute enough to next generation

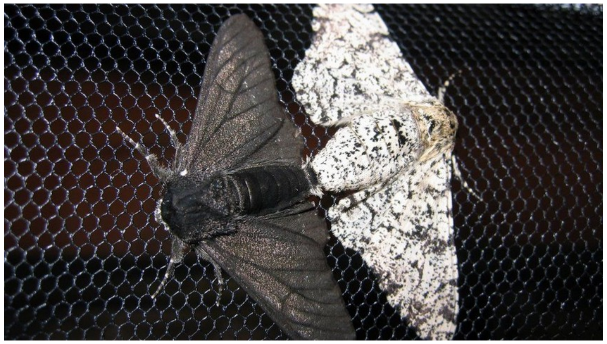
(a) **Stabilizing selection**

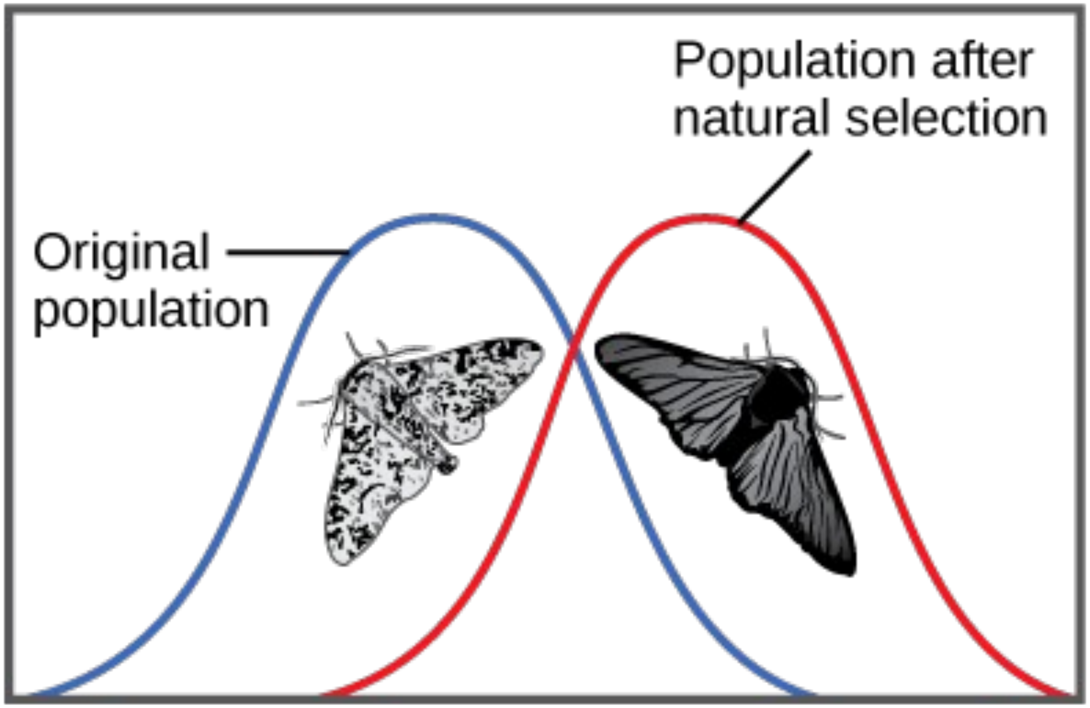


Robins typically lay four eggs, an example of stabilizing selection. Larger clutches may result in malnourished chicks, while smaller clutches may result in no viable offspring.

Directional selection

- Individuals at one extreme of a phenotypic range have greater reproductive success in a particular environment
- Initiators
  - ☐New allele with higher fitness introduced
  - ☐Prolonged environmental change



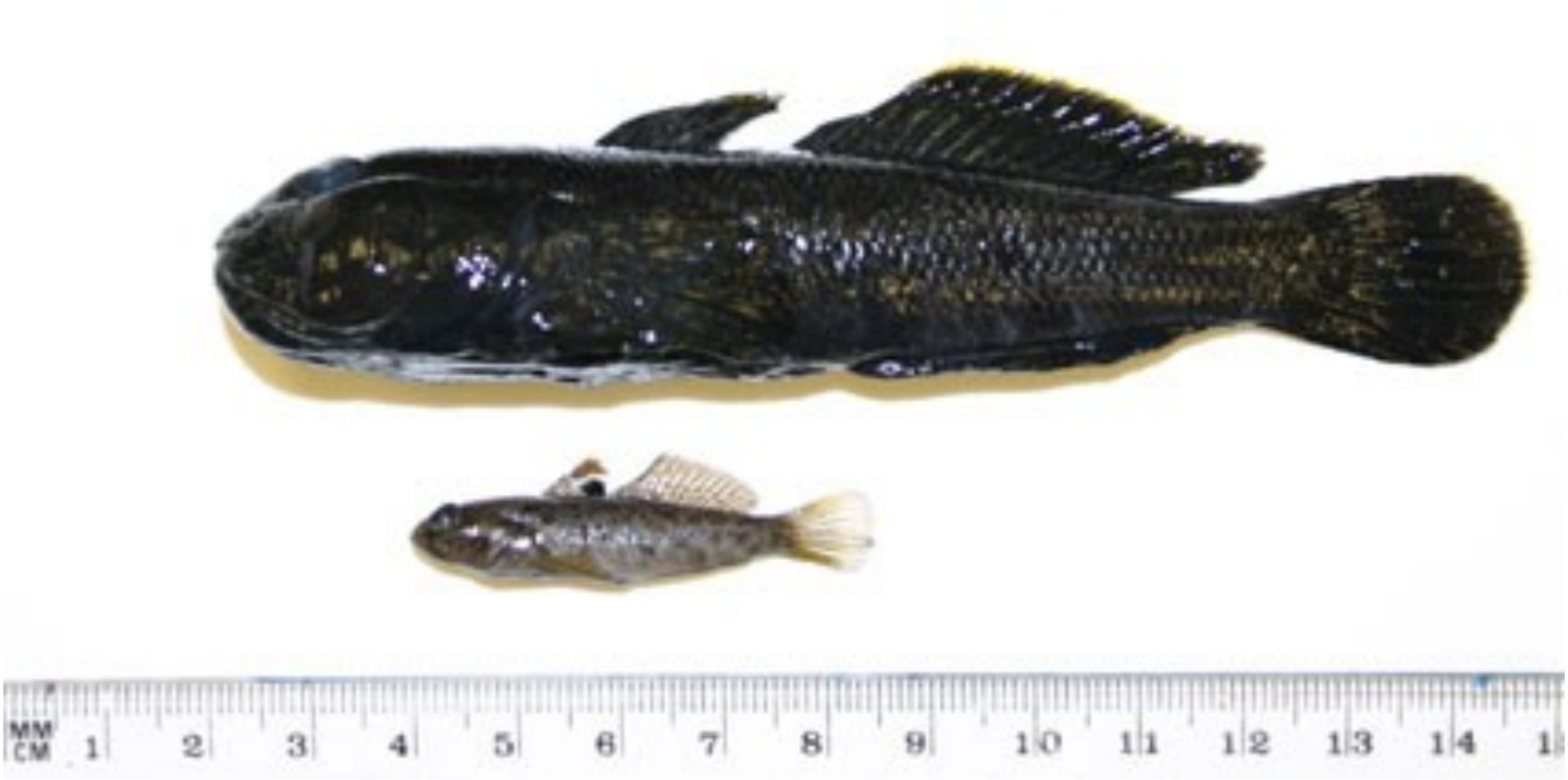

(b) **Directional selection**

Light-colored peppered moths are better camouflaged against a pristine environment; likewise, dark-colored peppered moths are better camouflaged against a sooty environment. Thus, as the Industrial Revolution progressed in nineteenth-century England, the color of the moth population shifted from light to dark, an example of directional selection.

Disruptive/Diversifying selection

- Favors the survival of two or more different genotypes (extreme values) that produce different phenotypes
- Likely to occur in populations that occupy heterogeneous environments
- Members of the populations can freely interbreed
- Ex. Goby fish males

Round Goby Fish (disruptive selection)

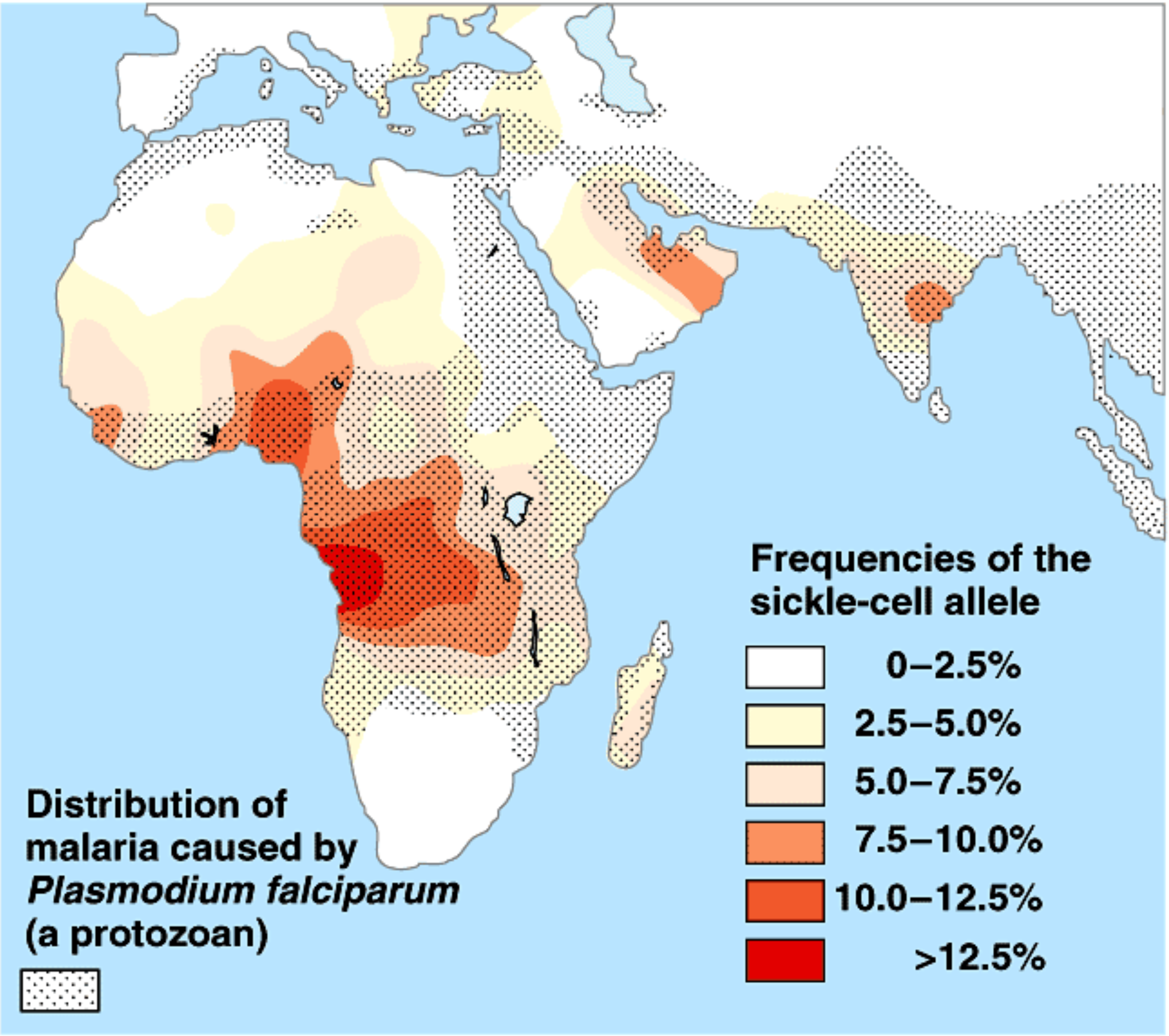


The parental male is the big fish in this picture and the sneaker male is the small fish. https://blog.nationalgeographic.org/2009/06/16/round-goby-fish-have-two-kinds-of-males-scientists-discover/

Balancing selection

- Maintains genetic diversity
- Balanced polymorphism
  - ❑Two or more alleles are kept in balance, and therefore are maintained in a population over the course of many generations
  - ❑Also known as **heterozygote advantage** (sickle cell anemia allele)

Mapping malaria and the sickle-cell allele


Frequencies of the sickle-cell allele
0–2.5%
2.5–5.0%
5.0–7.5%
7.5–10.0%
10.0–12.5%
>12.5%
Distribution of malaria caused by *Plasmodium falciparum* (a protozoan)

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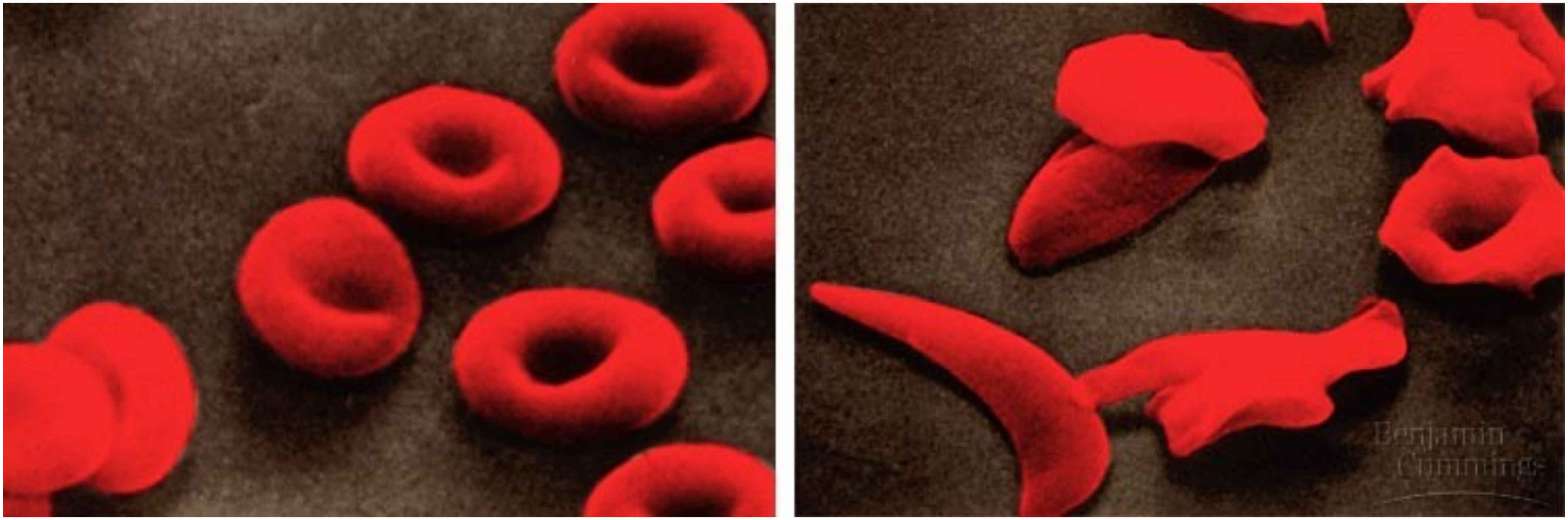
Normal and sickled erythrocytes (red blood cells)

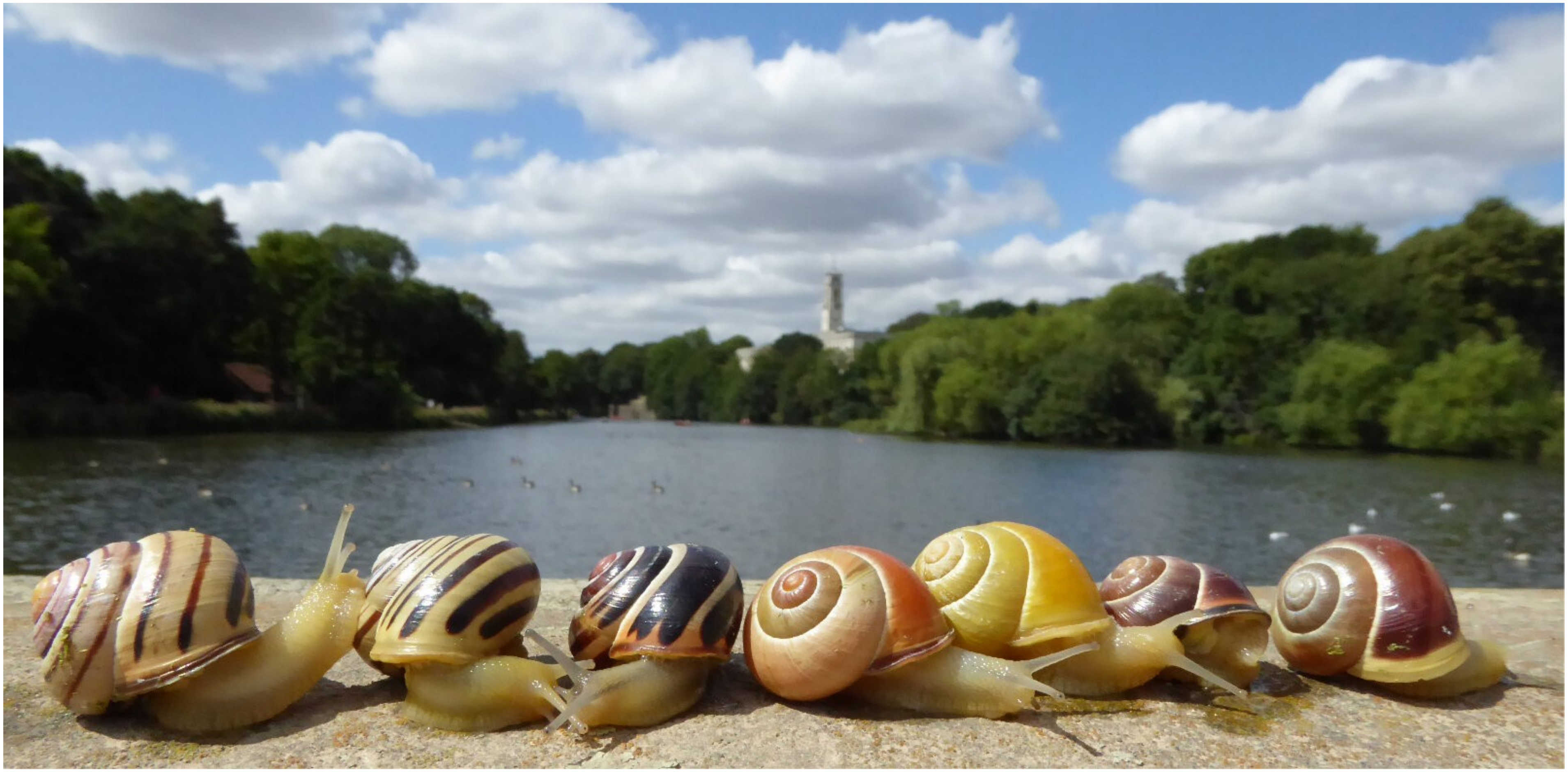


Frequency dependent selection – a type of balancing selection

- Side-blotched lizards.
- https://youtu.be/rafdHxBwIbQ (3.25)
- **Frequency-dependent selection** favors phe that are either common (positive frequency-dependent selection) or rare (negative frequency-dependent selection).
- Males play a game of rock-paper-scissors. Orange a big bully. Blue a steady mating partner. Yellow small and sneaky. Female choice prefers least common color.

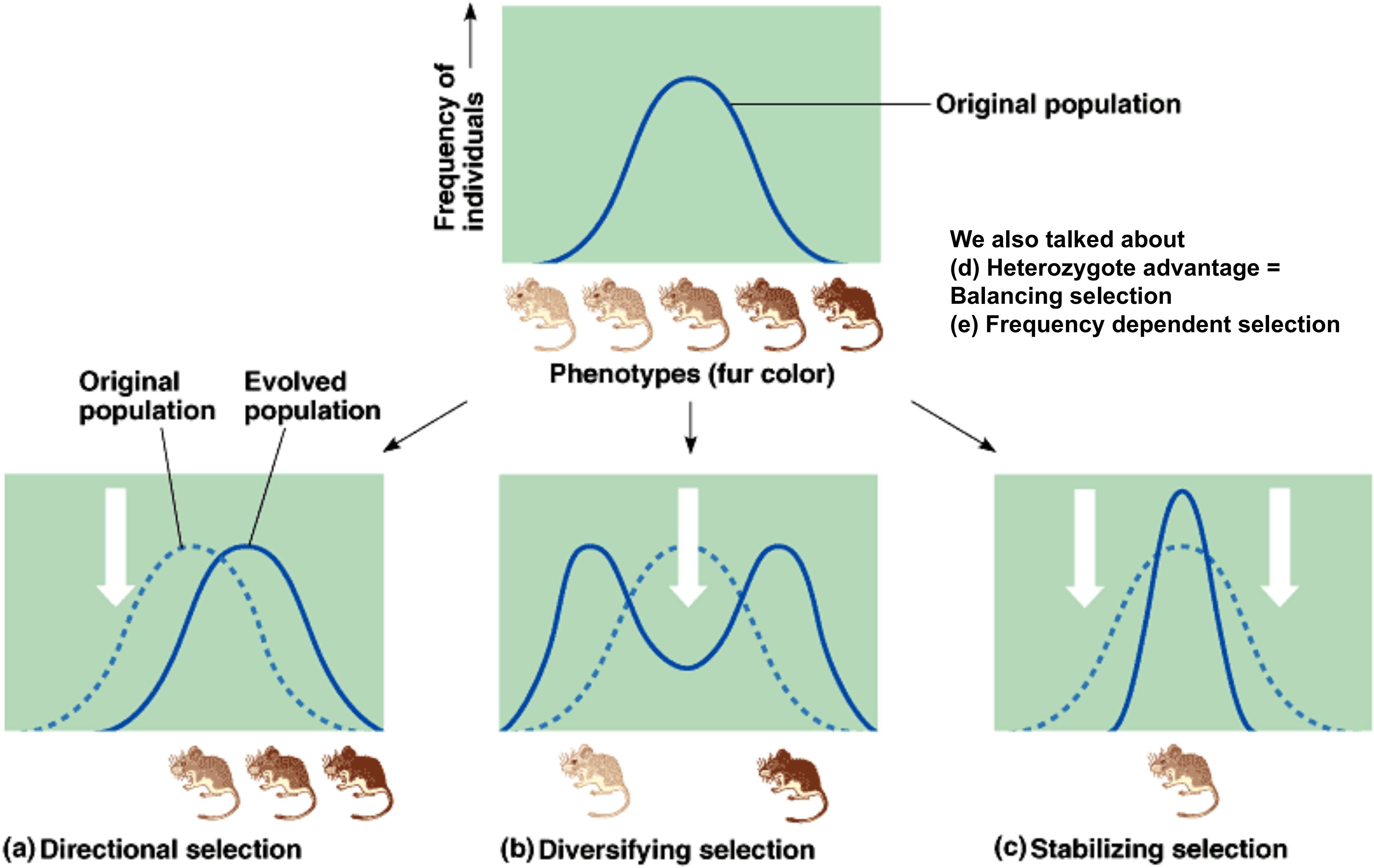
Side blotched lizards

Cepaea nemoralis: *an* example of negative frequency dependent selection



https://phys.org/news/2019-02-humans-struggle-snail-shell-technology.html

Modes of selection - summary



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We also talked about
(d) Heterozygote advantage = Balancing selection
(e) Frequency dependent selection

Also called disruptive

Sexual Selection (non-random mating)

- Form of natural selection
- Directed at certain traits of sexually reproducing species that make it more likely for individuals to find or choose a mate and/or engage in successful mating
- This could lead to any of the modes of selection we have already discussed (but directional selection occurs when females choose extreme traits.

- **Intrasexual selection**
  - Between members of the same sex
  - Horns in male sheep, antlers in male moose, male fiddler crab enlarged claws
  - Males directly compete for mating opportunities or territories
- **Intersexual selection**
  - Between members of the opposite sex
  - Female choice
  - Often results in showy characteristics for males
  - Cryptic female choice
    - Genital tract or egg selects against genetically related sperm
      - Inhibits inbreeding

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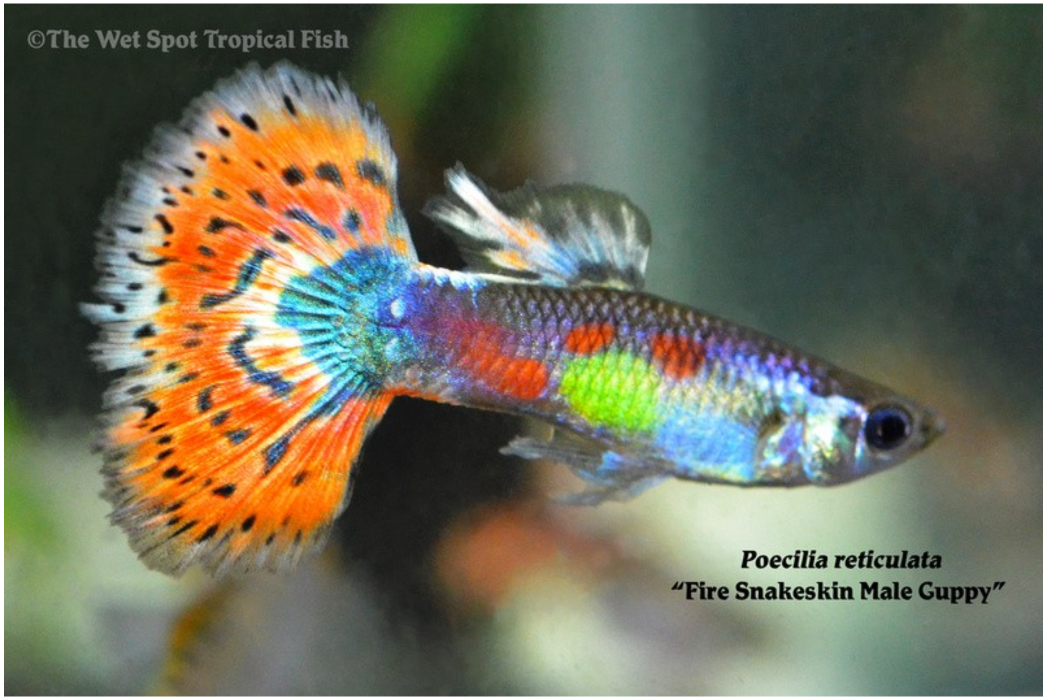
(a) Intrasexual selection

(b) Intersexual selection

(c) Sexual selection balanced by predation

a: © Gerald Cubitt; b: © Topham/The Image Works; c: © Photo by Darren P. Croft, University of Exeter UK

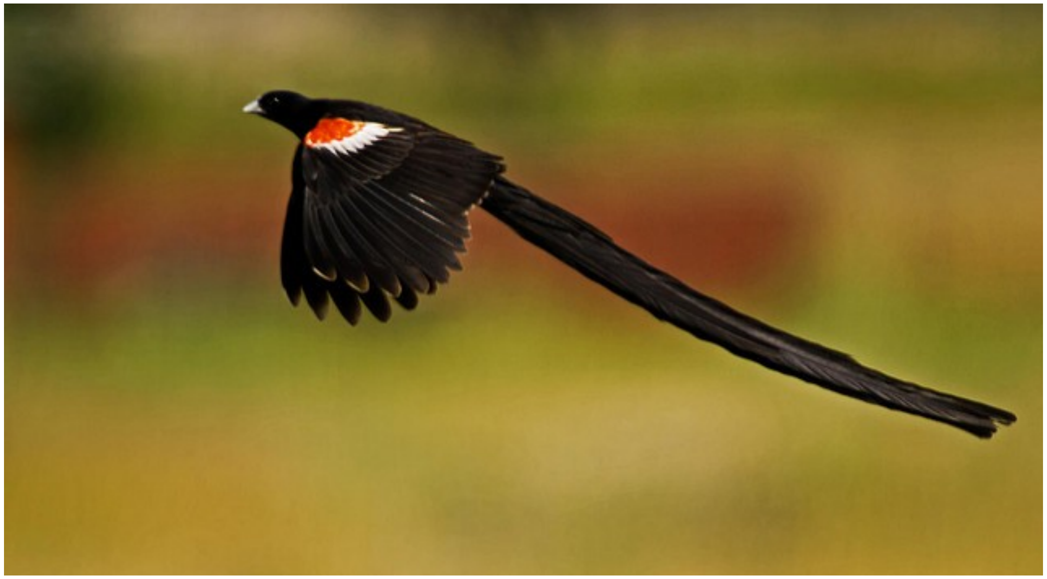
- Explains traits that decrease survival but increase reproductive success
- ex: **Guppy, *Poecilia reticulata*** – Male is brightly colored compared to the female
- Females prefer brightly colored males

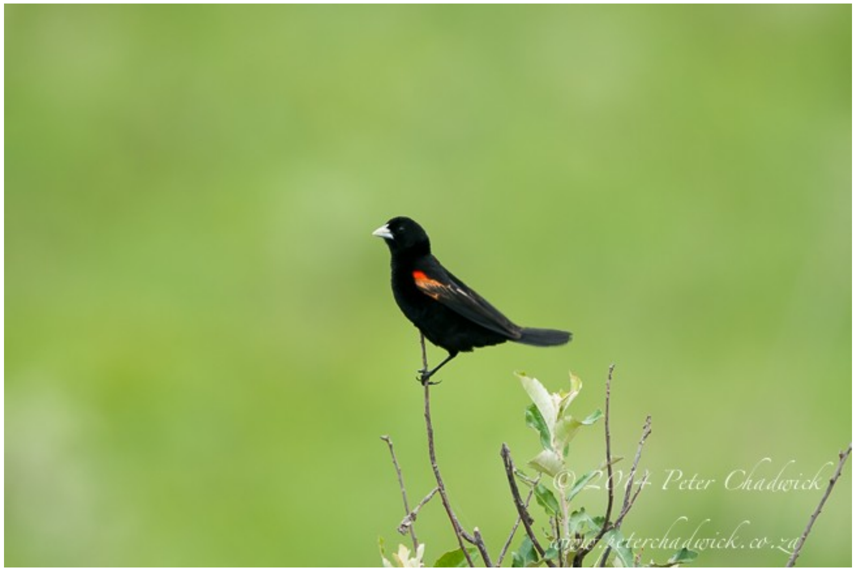


- In places with **few predators,** the males tend to be brightly colored
- In places where predators are **abundant,** brightly colored males are less plentiful because they are subject to predation

- Relative abundance of brightly and dully colored males depends on the **balance** between sexual selection, which favors bright coloring, and escape from predation, which favors dull coloring. Cost benefit approach.

Widowbirds





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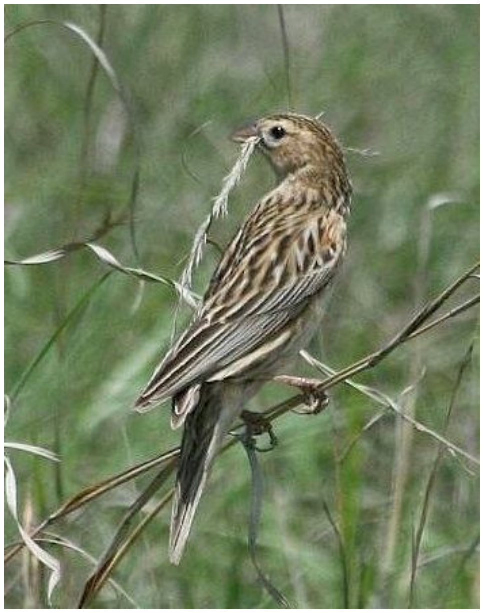

Genetic Drift

- Changes allelic frequency due to **random chance (random sampling)**
- Random events **unrelated to fitness**
- The allele is generally either **lost** or **fixed**
- Frequency reaches 0% or 100%
- Faster in smaller populations

Bottleneck (1 type of genetic drift)

- Population reduced dramatically and then rebuilds
- Randomly eliminates members without regard to genotype
- Surviving members may have allele frequencies different from original population
- Allele frequencies can drift substantially when population is small
- New population likely to have **less genetic variation**
- “In one fell swoop, the genetic structure of the survivors becomes the genetic structure of the entire population, which may be very different from the pre-disaster population.” Openstax

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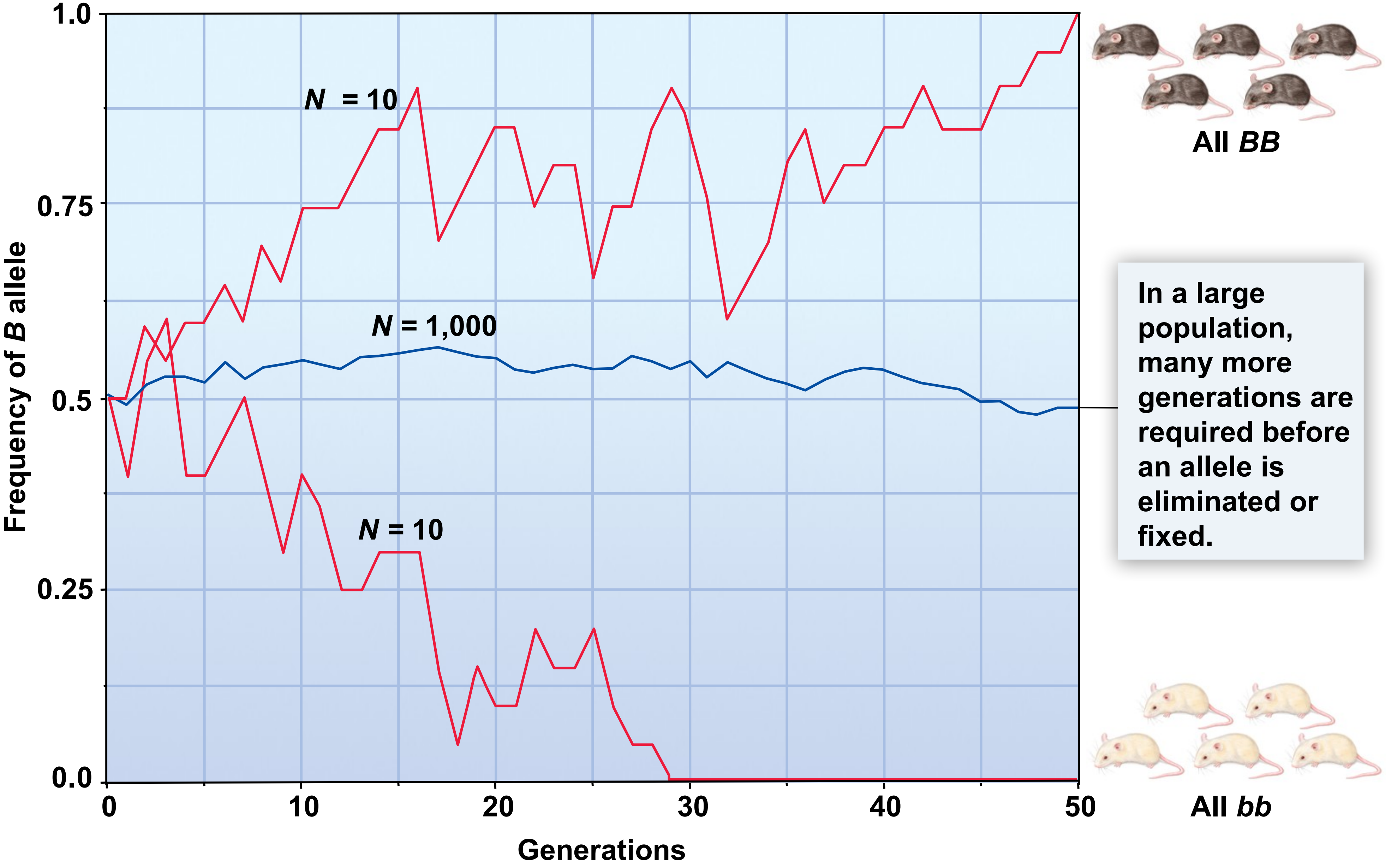
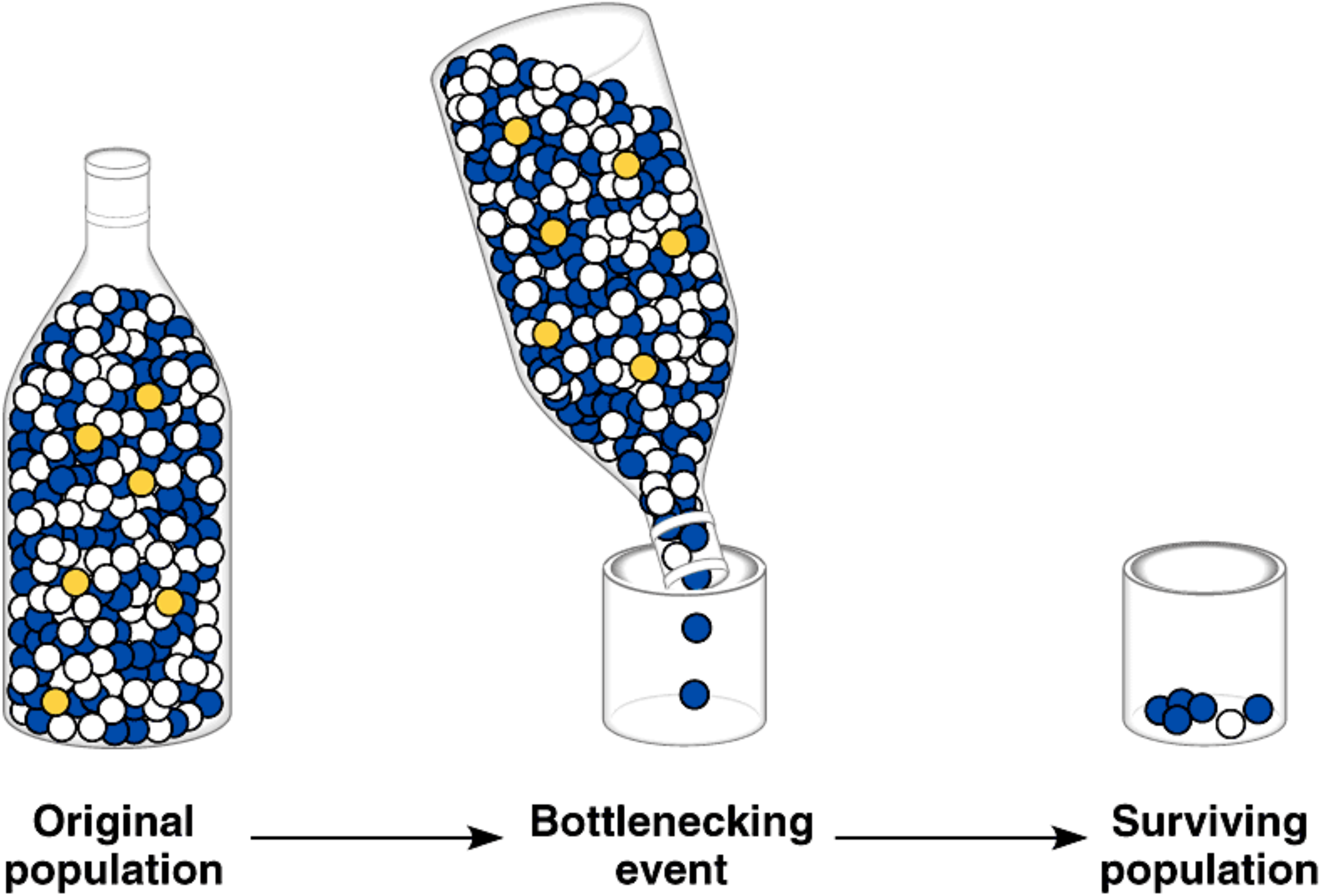


In a large population, many more generations are required before an allele is eliminated or fixed.

The bottleneck effect



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Cheetahs, the bottleneck effect (10,000 years ago – end of ice age, plus poaching and habitat loss.)

http://evolution.berkeley.edu/evolibrary
/news/070701_cheetah

Addo elephants of South Africa

Addo elephants

- Originally a large population with an uncommon allele for reduced or absent tusks in females only.
- Population reduced to 11 individuals by 1930, after a power hunter was contracted to kill all the local population by farmers. This was composed of 8 females and 3 males.
- Park established to protect remaining elephants.
- Population is now up to 324, all due to reproduction, no immigration.

Founder effect (another type of genetic drift)

- Small group of individuals separates from a larger population and establishes a **new population**

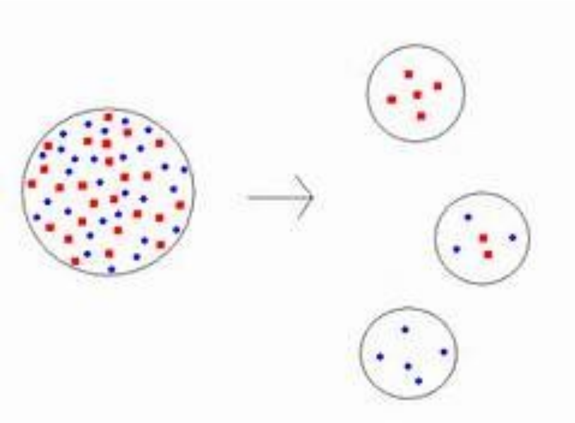
- Relatively small founding population expected to have less genetic variation than original population

- Allele frequencies in founding population may differ markedly from original population

- Similar consequences to a bottleneck

- Darwin's finches blown over to the Galapagos

- Canadian goose/Hawaiian goose



Migration and Nonrandom Mating

- **Gene flow** occurs when individuals migrate between populations having different allele frequencies
- Migration tends to **reduce differences** in allele frequencies between the two populations
- Tends to enhance genetic diversity within a population

Gene flow and human evolution

- **Gene flow tends to reduce differences between populations**
- **Gene flow is accelerated with increases in migration rates**
- **May lead to population coalescence**

SPECIAL ISSUE
TIME
Take a good look at this woman. She was created by a computer from a mix of several races. What you see is a remarkable preview of . . .
THE NEW FACE OF AMERICA
How Immigrants Are Shaping the World's First Multicultural Society
Benjamin Cummings

Nonrandom mating

- One of the conditions required to establish the Hardy-Weinberg equilibrium is **random mating**
  - Individuals choose their mates irrespective of their genotypes and phenotypes
- Forms of nonrandom mating
  - **Assortative / disassortative mating**
  - **Inbreeding**

- **Assortative mating (homogamy)**
    - ❑Individuals with similar phenotypes are more likely to mate (color, body size, human royals)
    - ❑Increases the proportion of homozygotes
- **Disassortative mating (heterogamy)**
    - ❑Dissimilar phenotypes mate preferentially
    - ❑Favors heterozygosity (maintains variation)

- **Inbreeding**
  - ❑Choice of mate based on genetic history
  - ❑Does not favor any particular allele but does increase the likelihood the individual will be homozygous
  - ❑May have negative consequences with regard to recessive alleles
  - ❑Lower mean fitness of a population if homozygous offspring have a lower fitness value
  - ❑INBREEDING DEPRESSION

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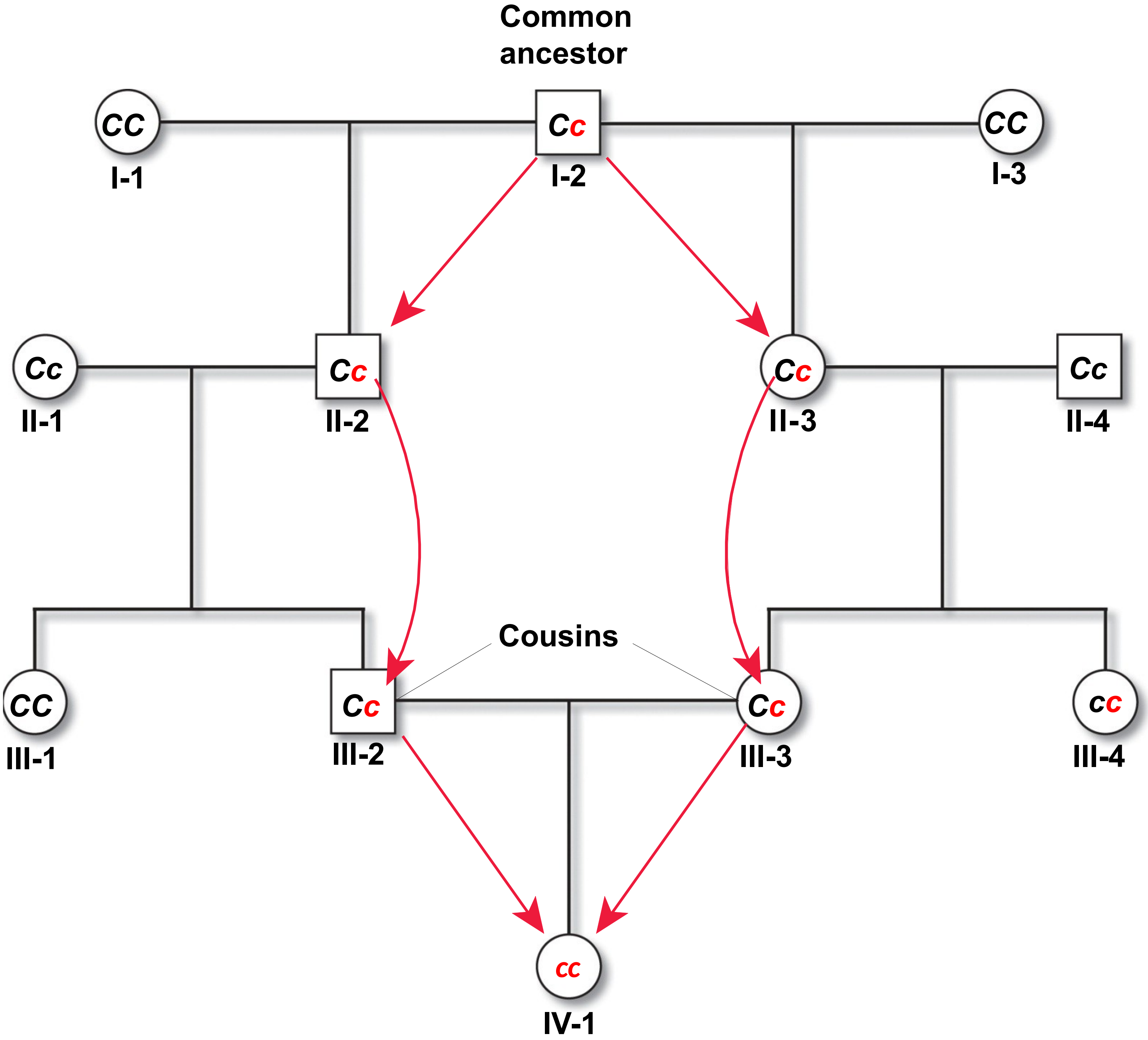


If 36% of an African population is born with a severe form of sickle-cell anemia (ss), what percentage of the population will be more resistant to malaria because they are heterozygous(Ss) for the sickle-cell gene?

Show your work. You are solving for Genotype frequency of the heterozygote.

0.36 genotype frequency

Allele frequency (s) = square root of 0.36 = 0.6 =q

p+q=1. p=0.4

2pq = 2x0.4x0.6 = 0.48

SS frequency = 0.16

0.16 + 0.48 + 0.36 = 1

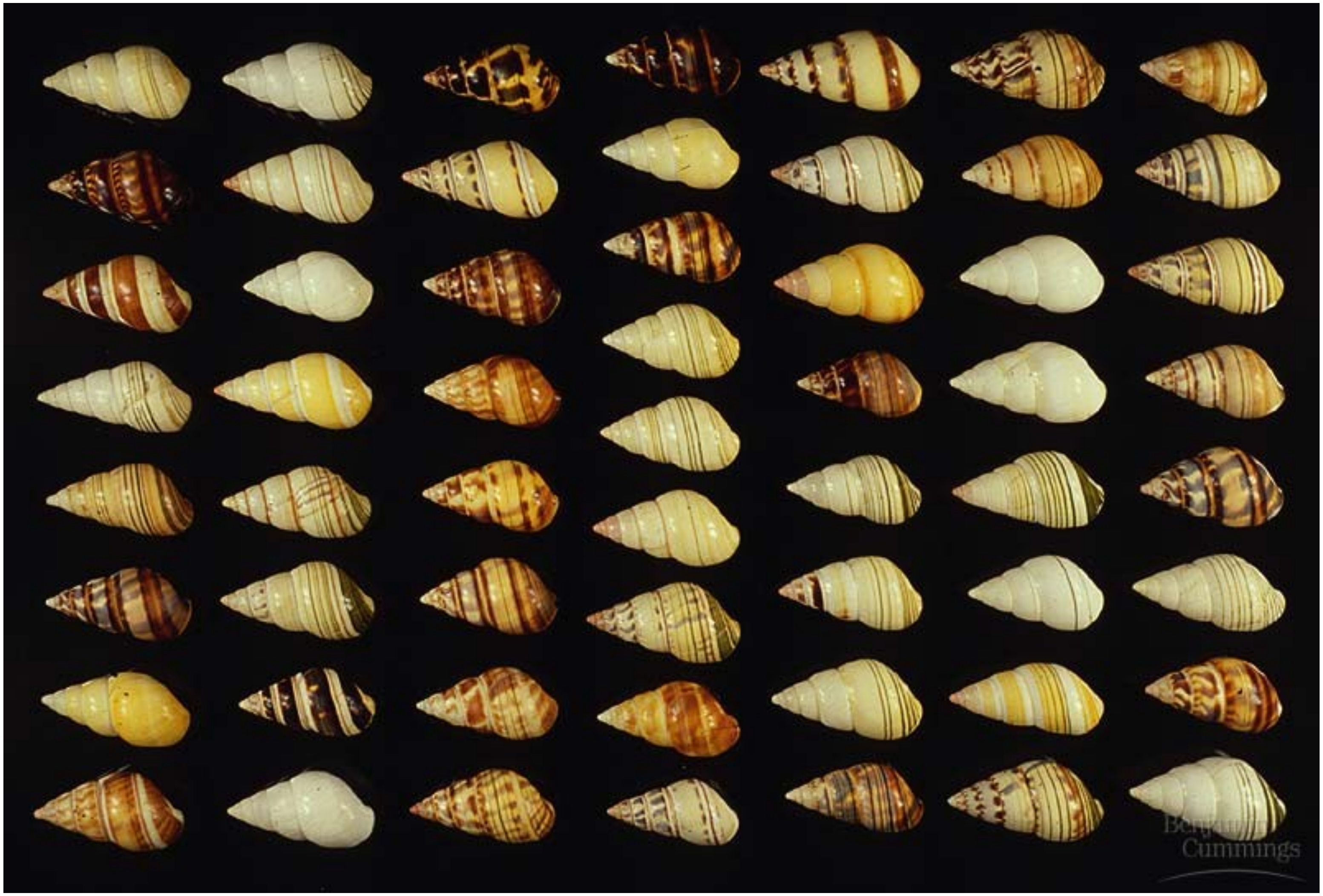
Hardy-Weinberg

Evolution in Populations

Evolution in Populations

- **Population genetics** – study of the genetic variation within and between populations
- Population – localized group of individuals of the **same species**
- **Individual organisms do NOT evolve: populations DO**
- **Gene Pool** – total of all alleles (genes) within a population
- **Gene Flow** – movement of alleles within and between populations

Shells: all the same species (*Liguus fascitus*)



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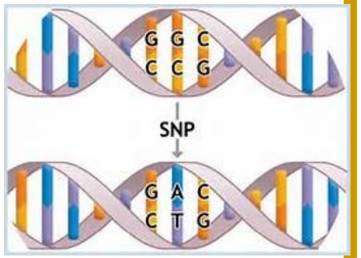
Genes Are Usually Polymorphic

- Polymorphism – traits display variation within a population
    - Due to two or more alleles that influence phenotype
- **Polymorphic gene** – two or more alleles
- **Monomorphic gene** – predominantly single allele
- **Single nucleotide polymorphisms (SNPs)**
    - Smallest type of genetic change in a gene
    - Most common – 90% of variation in human gene sequences
- Large, healthy populations exhibit a high level of genetic diversity
- Raw material for evolution



Allele and genotype frequencies

- Related but distinct calculations
- Think of frequency as a **percentage**

$$\text{Allele frequency} = \frac{\text{Number of copies of a specific allele in a population}}{\text{Total number of all alleles for that gene in a population}}$$

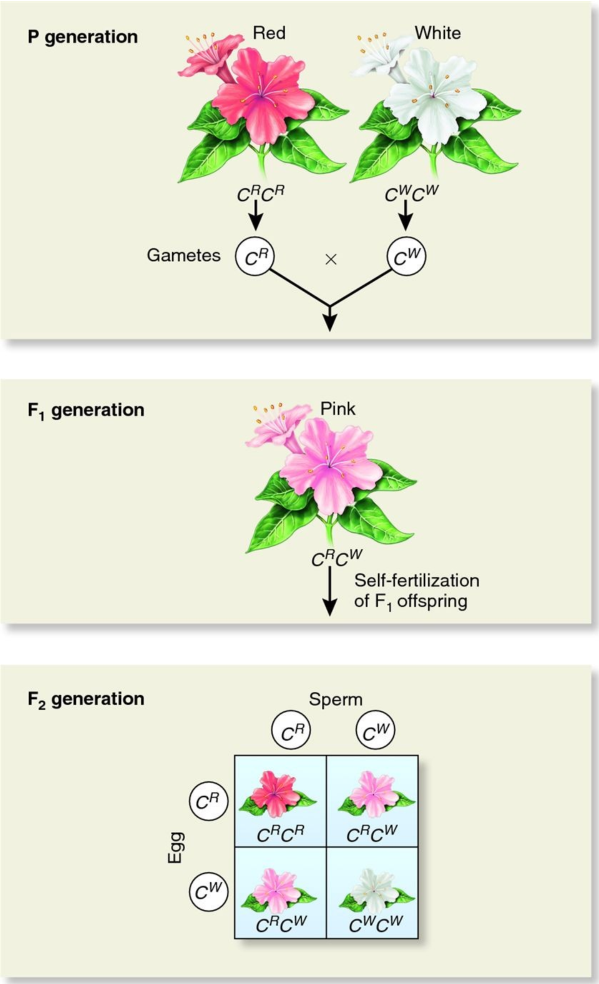
$$\text{Genotype frequency} = \frac{\text{Number of individuals with a particular genotype in a population}}{\text{Total number of individuals in a population}}$$

Example: Four o’clock plants

49 red-flowered plants with the genotype C^RC^R

42 pink-flowered plants with the genotype C^RC^W

9 white-flowered plants with the genotype C^WC^W



Statement of Hardy-Weinberg

BI-ALLELIC SYSTEM

- p = frequency of one allele in the population (say C^R)

Statement of Hardy-Weinberg

BI-ALLELIC SYSTEM

- p = frequency of one allele in the population (say C^R)
- q = frequency of the other allele (C^W)

Statement of Hardy-Weinberg

BI-ALLELIC SYSTEM

- p = frequency of one allele in the population (say C^R)
- q = frequency of the other allele (C^w)
- p + q = 1 (%p + %q = 100%)

Statement of Hardy-Weinberg

BI-ALLELIC SYSTEM

- p = frequency of one allele in the population (say C^R)
- q = frequency of the other allele (C^w)
- $p + q = 1$ (%p + %q = 100%)
- p^2 = frequency of C^RC^R genotype (homozygous dominant)

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- q^2 = frequency of C^WC^W genotype (homozygous recessive)

Statement of Hardy-Weinberg

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- p = frequency of one allele in the population (say C^R)
- q = frequency of the other allele (C^w)
- p + q = 1 (%p + %q = 100%)
- p^2 = frequency of C^RC^R genotype (homozygous dominant)
- q^2 = frequency of C^WC^W genotype (homozygous recessive)
- 2pq = frequency of C^RC^W genotype (heterozygote)

Hardy-Weinberg equation

$$p^2 + 2pq + q^2 = 1$$

p^2 = the genotype frequency of C^RC^R homozygotes Red homozygotes

$2pq$ = the genotype frequency of C^RC^W heterozygotes Pink heterozygotes

q^2 = the genotype frequency of C^WC^W homozygotes White homozygotes

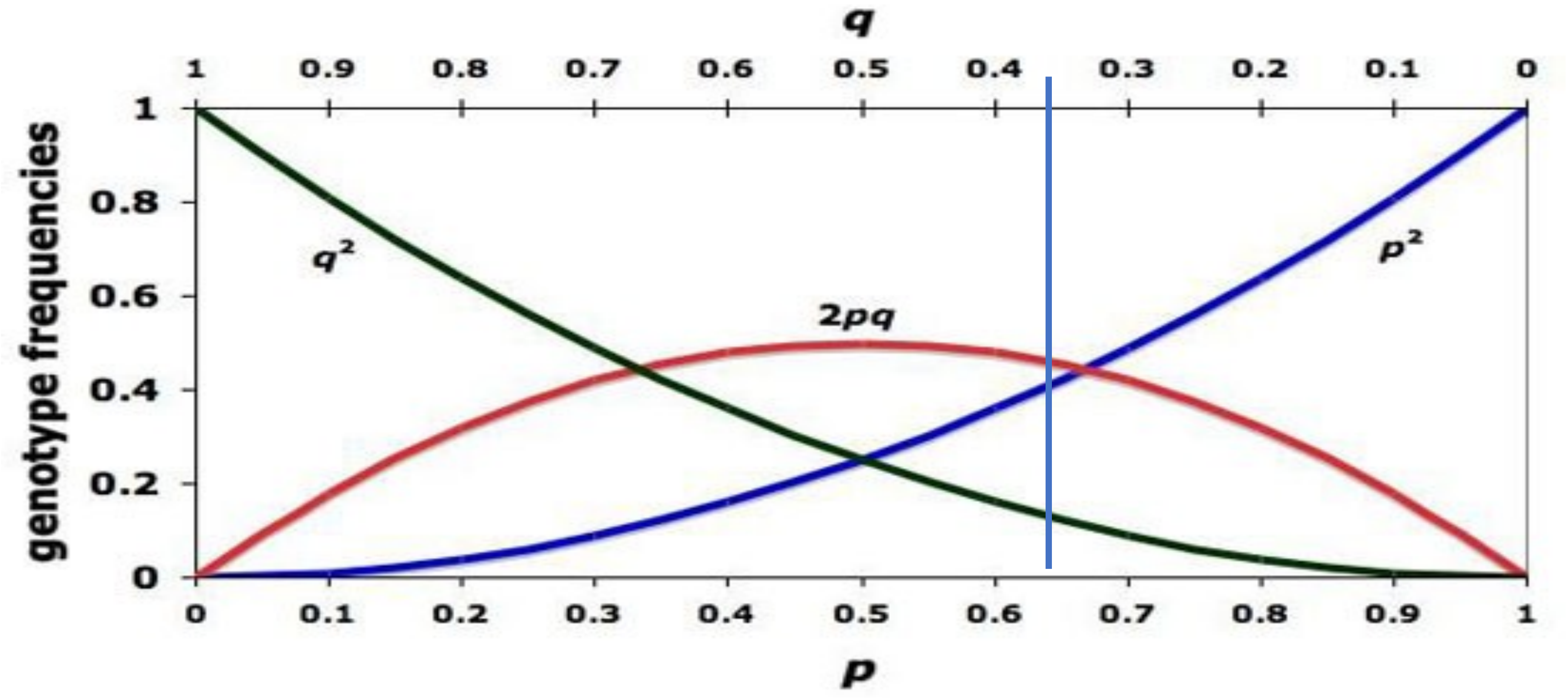
If $p = 0.7$ and $q = 0.3$, then

Frequency of $C^RC^R = p^2 = (0.7)^2 = 0.49$

Frequency of $C^RC^W = 2pq = 2(0.7)(0.3) = 0.42$

Frequency of $C^WC^W = q^2 = (0.3)^2 = 0.09$

Hardy Weinberg allele and genotype frequencies

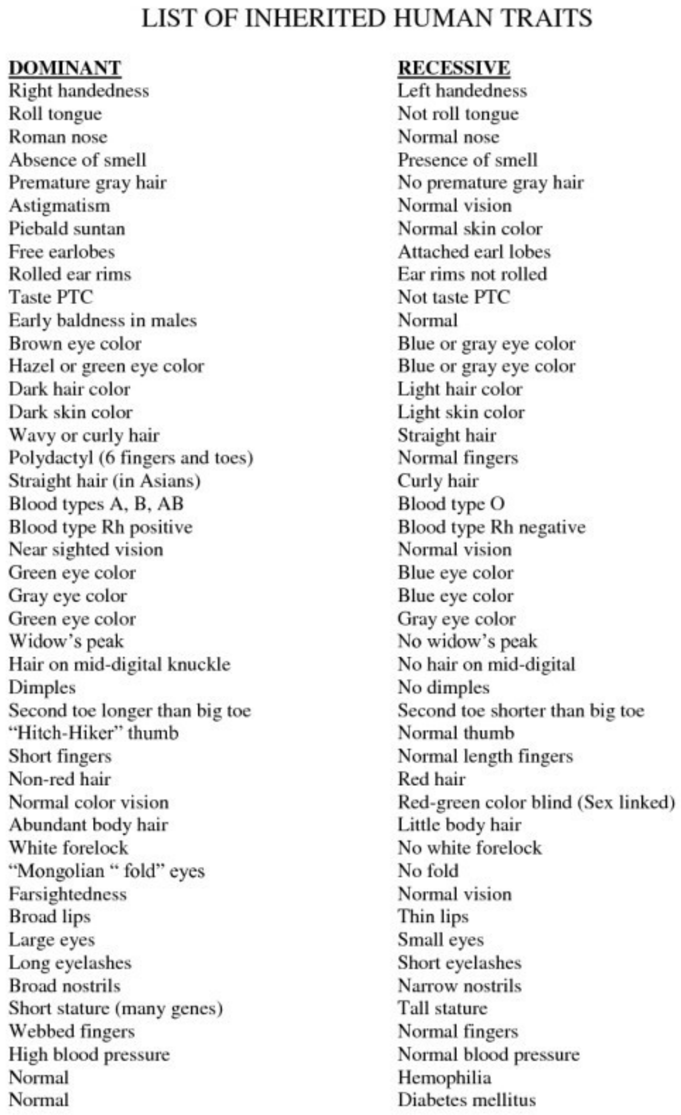


	Female gamete **A** (p)	Female gamete **a** (q)
Male gamete **A** (p)	**AA** (p^2)	**Aa** (pq)
Male gamete **a** (q)	**Aa** (pq)	**aa** (q^2)

Frequency of **AA** = p^2

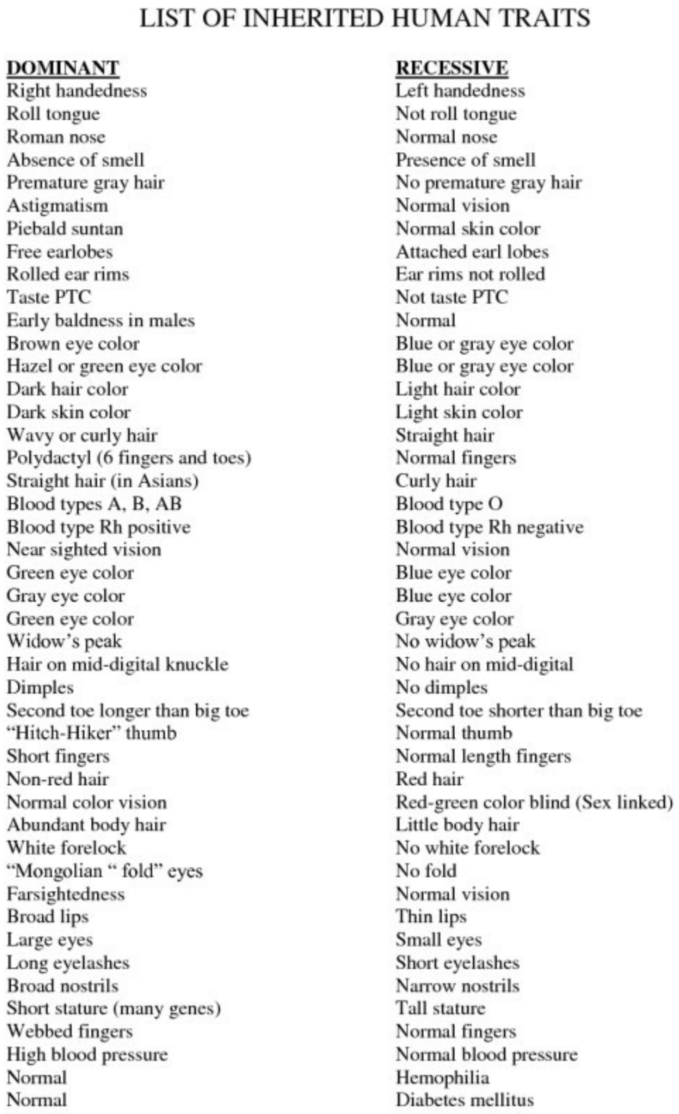
Frequency of **Aa** = $2pq$

Frequency of **aa** = q^2



LIST OF INHERITED HUMAN TRAITS

DOMINANT	**RECESSIVE**
Right handedness	Left handedness
Roll tongue	Not roll tongue
Roman nose	Normal nose
Absence of smell	Presence of smell
Premature gray hair	No premature gray hair
Astigmatism	Normal vision
Piebald suntan	Normal skin color
Free earlobes	Attached earl lobes
Rolled ear rims	Ear rims not rolled
Taste PTC	Not taste PTC
Early baldness in males	Normal
Brown eye color	Blue or gray eye color
Hazel or green eye color	Blue or gray eye color
Dark hair color	Light hair color
Dark skin color	Light skin color
Wavy or curly hair	Straight hair
Polydactyl (6 fingers and toes)	Normal fingers
Straight hair (in Asians)	Curly hair
Blood types A, B, AB	Blood type O
Blood type Rh positive	Blood type Rh negative
Near sighted vision	Normal vision
Green eye color	Blue eye color
Gray eye color	Blue eye color
Green eye color	Gray eye color
Widow's peak	No widow's peak
Hair on mid-digital knuckle	No hair on mid-digital
Dimples	No dimples
Second toe longer than big toe	Second toe shorter than big toe
"Hitch-Hiker" thumb	Normal thumb
Short fingers	Normal length fingers
Non-red hair	Red hair
Normal color vision	Red-green color blind (Sex linked)
Abundant body hair	Little body hair
White forelock	No white forelock
"Mongolian " fold" eyes	No fold
Farsightedness	Normal vision
Broad lips	Thin lips
Large eyes	Small eyes
Long eyelashes	Short eyelashes
Broad nostrils	Narrow nostrils
Short stature (many genes)	Tall stature
Webbed fingers	Normal fingers
High blood pressure	Normal blood pressure
Normal	Hemophilia
Normal	Diabetes mellitus



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Short stature (many genes)	Tall stature
Webbed fingers	Normal fingers
High blood pressure	Normal blood pressure
Normal	Hemophilia
Normal	Diabetes mellitus

Widow’s peak

- This is a dominant trait.

Widow’s peak (dominant) Zoom poll

- How many # students in the class? 134
- How many student’s do NOT have widow’s peak? 107

Frequency or proportion of this recessive genotype (q^2)? 107/134 = 80% = 0.8

Widow’s peak (dominant) Zoom poll

- How many # students in the class?
- How many student’s do NOT have widow’s peak?
- Not having widow’s peak is the recessive trait, so what is their genotype? We will use W=widow’s peak allele and w =no widow’s peak allele.
- What is the **genotype** frequency of ww? 0.80
- If p=frequency of W, and q =frequency of w, how can you calculate the frequency of q? **-->**

Widow's peak (dominant) Zoom poll

- How many # students in the class? A=134
- How many student's do NOT have widow's peak? B=107

Genotype frequency (ww) = B/A =%= (80%) = 0.8

ww $= q^2 = 0.8$

Widow’s peak (dominant) Zoom poll

- How many # students in the class? B
- How many student’s do NOT have widow’s peak? A

Genotype frequency (*ww*) = B/A =0.xx = q2 = 0.8

So, what is the **allele frequency** for q?

Take the square root of q^2 (*ww)* =?

Square root of 0.80 = 0.89 (89%) = q

1 - q = 1-.89 = **0.11 = p**

Widow's peak
# total, # yes, # no

- What did you calculate for q?
    - How did you get this?
- What did you calculate for p? 1-q
    - How did you get this?
- How do you solve for genotype frequencies?
- Start with genotype frequency for **homozogous recessives** in class (those without widow's peak)

Widow’s Peak

- Allele frequencies q=? p=?
  - p + q = 1 (p and q are percentages in decimal form) { %p + %q = 100%}
- Genotype frequencies
  - $P^2 + 2pq + q^2 = 1$ { $\%p^2 + \%2pq + \%q^2 = 100\%$}
    - P^2 = frequency of homozygous dominants ?
    - **q^2** = frequency of homozygous **recessives ?**
    - 2pq = frequency of heterozygotes = ?
    - Check your work: Do they add up to 1?
  - P^2 = homozygous dominant genotype frequency $(0.11)^2$

  = 0.11 x 0.11 = 0.01. $q^2 = 0.8$
  - heterozygote genotype freq. (2pq) = 2 x 0.89 x 0.11=0.19

Review for class data

- 134 students, 107 non-widow’s peak
- 107/134 = 0.8 genotype frequency for homozygous recessive
- sq. rt of 0.8 = **0.89 = q** allele frequency for recessive allele
- p+q=1, so 1-0.89 = **0.11 = p** or allele frequency of dominant allele
- $P^2 + 2pq + q^2 = 1$
- 0.01+0.19+0.80= 1

Finish Hardy-Weinberg

Patterns of Natural Selection

Review for class data

- $p + q = 1$ $p^2 + 2pq + q^2 = 1$
- 134 students, 107 non-widow’s peak
- 107/134 = 0.8 genotype frequency for homozygous recessive
- sq. rt of 0.8 = **0.89 = q** allele frequency for recessive allele
- p+q=1, so 1-0.89 = **0.11 = p** or allele frequency of dominant allele
- $P^2 + 2pq + q^2 = 1$
- 0.01+0.19+0.80= 1

Hardy Weinberg Equation of Population Genetics

ASSUMPTIONS

1. Large population - to ensure no sampling error from one generation to the next
2. Random mating - no assortative mating or mating by genotype
3. No mutations
4. No migration between populations
5. No selection - all genotypes reproduce with equal success

STATES: If all of the above, **ALLELE** frequency **WILL NOT CHANGE** from generation to generation

Example Problem

- **If 9% of an African population is born with a severe form of sickle-cell anemia (ss), what percentage of the population will be more resistant to malaria because they are heterozygous(Ss) for the sickle-cell gene?**

Calculating the heterozygote genotype frequency

- 0.09=q^2 =homozygous recessive genotype frequency
- 9% = 0.09

$P^2 + 2pq + q^2 = 1$, $p + q = 1$

- $0.09=q^2$ =homozygous recessive genotype frequency
- q =0.3 = square root of 0.09 = allele frequency of q

$P^2 + 2pq + q^2 = 1$, $p + q = 1$

- 0.09=q^2 =homozygous recessive genotype frequency
- q =0.3 = square root of 0.09 = allele frequency of q
- p + q = 1, so p = 0.7 = allele frequency of p

$P^2 + 2pq + q^2 = 1, \quad p + q = 1$

- 0.09=q^2 =homozygous recessive genotype frequency
- q =0.3 = square root of 0.09 = allele frequency of q
- q + p = 1, so p = 0.7 = allele frequency of p
- What is p^2 ? 0.49 = homozygous dominant gen. freq.

$P^2 + 2pq + q^2 = 1, \quad p + q = 1$

- 0.09=q^2 =homozygous recessive genotype frequency
- q =0.3 = square root of 0.09 = allele frequency of q
- q + p = 1, so p = 0.7 = allele frequency of p
- What is p^2 ? 0.49 = homozygous dominant gen. freq.
- What is the heterozygote genotype frequency ?
- $p^2 + 2pq + q^2 = 1$ $\qquad$ $0.49 + 2pq + 0.09 = 1$
- 2pq = 0.42

$P^2 + 2pq + q^2 = 1$, $p + q = 1$

- $0.09=q^2$ =homozygous recessive genotype frequency
- $q = 0.3$ = square root of 0.09 = allele frequency of q
- $q + p = 1$, so $p = 0.7$ = allele frequency of p
- What is p^2 ? 0.49 = homozygous dominant gen. freq.
- What is the heterozygote genotype frequency ?
- $p^2 + 2pq + q^2 = 1$ $0.49 + 2pq + 0.09 = 1$
- $2pq = 0.42$
- 49% homo dominant, 9% homo recessive, 42% heterozygotes

What is the genotype frequency of the heterozygote? Solve for q, solve for p, plug into formula

- Suppose we had a population of 500 individuals, in which 36% of individuals were albino (albinism is a recessive characteristic = aa)
- Using the equations: $p + q = 1$ **and** $p^2 + 2pq + q^2 = 1$
- ● If q^2 = 0.36 ð $q = 0.6$ ($\sqrt{0.36}$)
- ● If $q = 0.6$ ð $p = 0.4$ ($p + 0.6 = 1$)
- ● If $p = 0.4$ ð p^2 = 0.16 (0.4×0.4)
- ● Therefore $2pq$ = 0.48 ($2 \times 0.4 \times 0.6$)

If not in Hardy-Weinberg equilibrium, why not? Maybe Natural Selection

- Phenotypic traits that are heritable, and give a survival or reproductive advantage to an individual, become more common in successive generations (think Galapagos finches)

- Over time, natural selection results in **adaptations -** changes in phenotypes and their underlying genotypes in populations of living organisms that promote their survival and reproduction in a particular environment

Natural selection does not act on individual alleles, however, but on entire organisms – the whole phenotype.

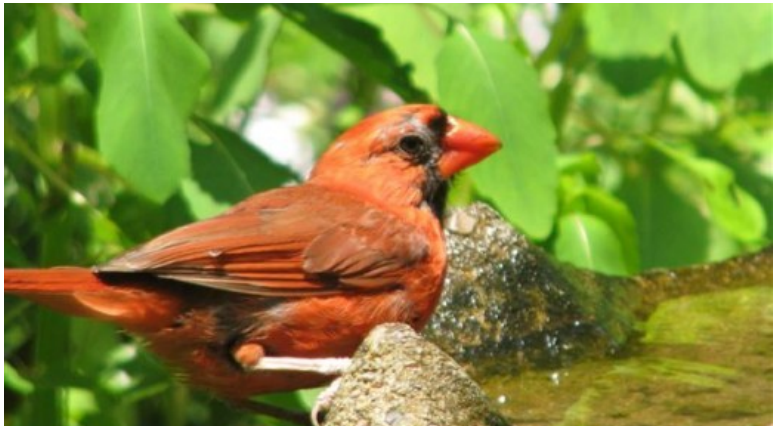
Populations evolve, not individuals.
Microevolution is measured in the population.
But, natural selection acts on individuals, not populations.

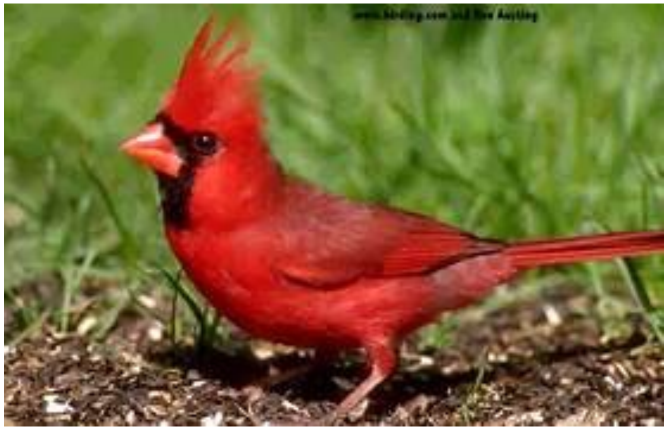
- **Reproductive success (fitness)**
  - Likelihood of an individual contributing fertile offspring to the next generation
  - Relative likelihood that a genotype will contribute to the gene pool of the next generation as compared to other genotypes

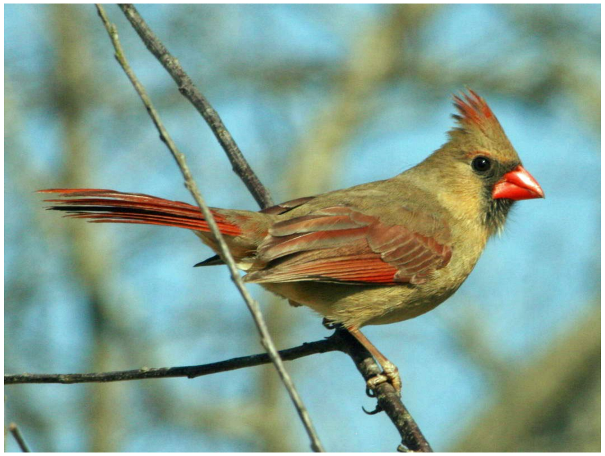
FITNESS

- Attributed to two categories of traits
    - Certain characteristics make organisms better adapted and more likely to **survive** to reproductive age
    - Traits may be directly associated with **reproduction**, such as ability to find a mate and ability to produce viable gametes and offspring

Cardinals







Modern description of natural selection (Darwin’s postulates re-stated)

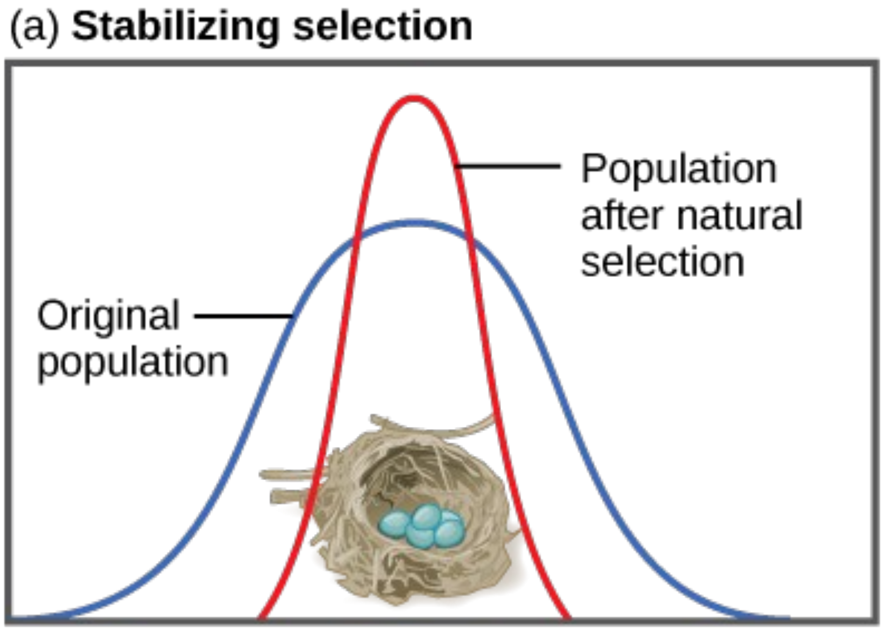
1. Within a population, allelic variation arises from random mutations that cause differences in DNA sequences
2. The products of some alleles enhance an individual’s survival or reproductive capability compared to other members of the population
3. Individuals with advantageous alleles are more likely to survive and contribute their alleles to the gene pool of the next generation
4. Over the course of many generations, allele frequencies of many different genes may change through natural selection, thereby significantly altering the characteristics of a population

Natural selection patterns – how does selection proceed?

- Stabilizing selection
- Directional selection
- Disruptive/Diversifying selection
- Frequency-dependent
- Balancing selection
- Sexual selection

Stabilizing selection

- Favors the survival of individuals with intermediate phenotypes
- Extreme values of a trait are selected against
- Clutch size
  - ❑Too many eggs and offspring – die due to lack of care and food
  - ❑Too few eggs – does not contribute enough to next generation


(a) **Stabilizing selection**
Population after natural selection
Original population

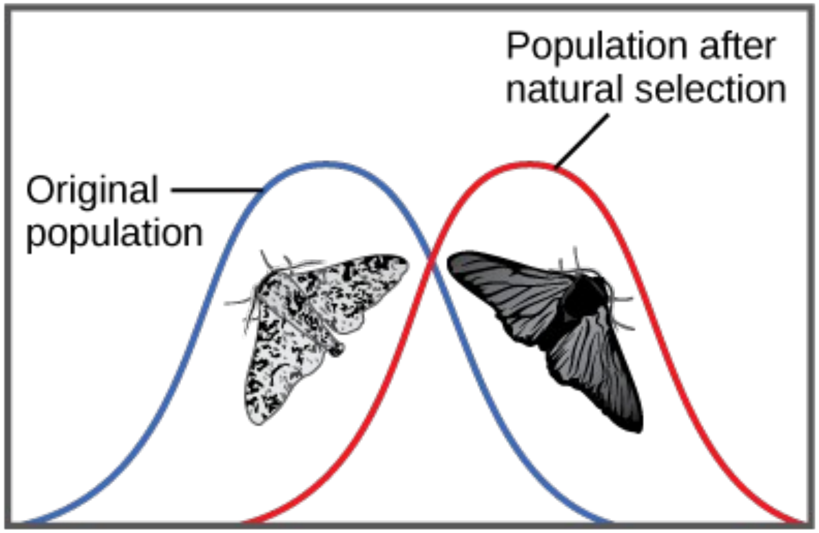
Robins typically lay four eggs, an example of stabilizing selection. Larger clutches may result in malnourished chicks, while smaller clutches may result in no viable offspring.

Directional selection

- Individuals at one extreme of a phenotypic range have greater reproductive success in a particular environment

- Initiators
  - ❑New allele with higher fitness introduced
  - ❑Prolonged environmental change

(b) **Directional selection**

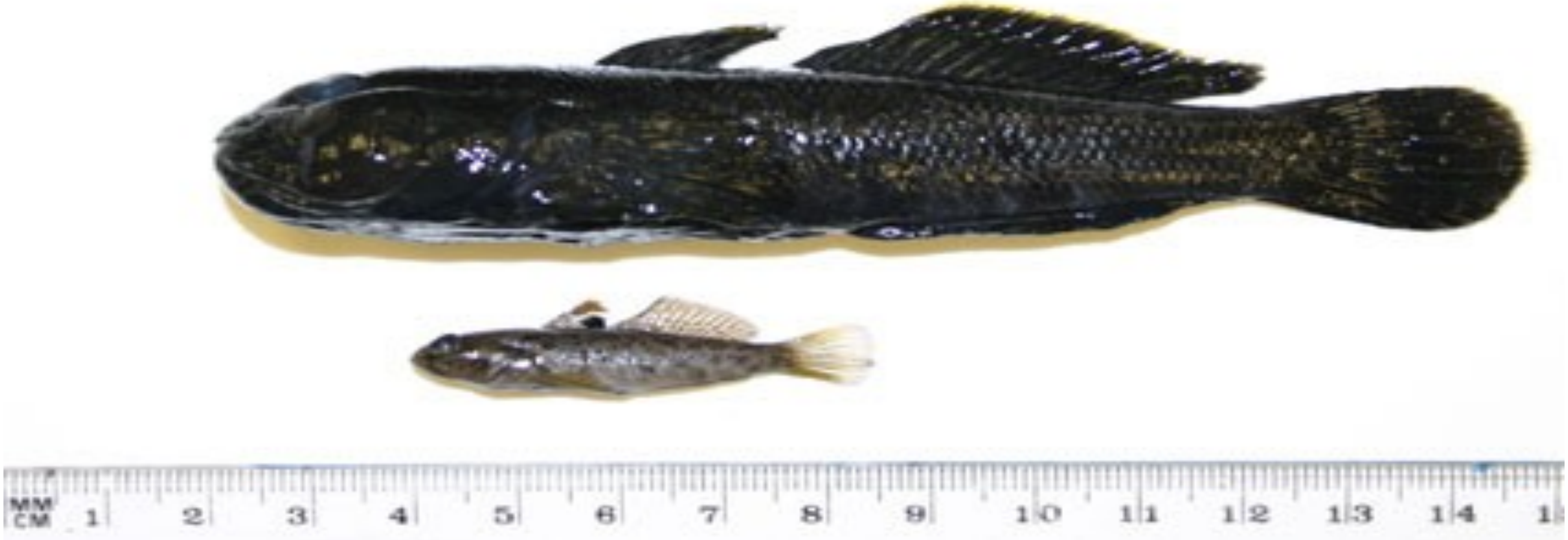


Light-colored peppered moths are better camouflaged against a pristine environment; likewise, dark-colored peppered moths are better camouflaged against a sooty environment. Thus, as the Industrial Revolution progressed in nineteenth-century England, the color of the moth population shifted from light to dark, an example of directional selection.

Disruptive/Diversifying selection

- Favors the survival of two or more different genotypes (extreme values) that produce different phenotypes
- Likely to occur in populations that occupy heterogeneous environments
- Members of the populations can freely interbreed
- Ex. Goby fish males

Round Goby Fish (disruptive selection)

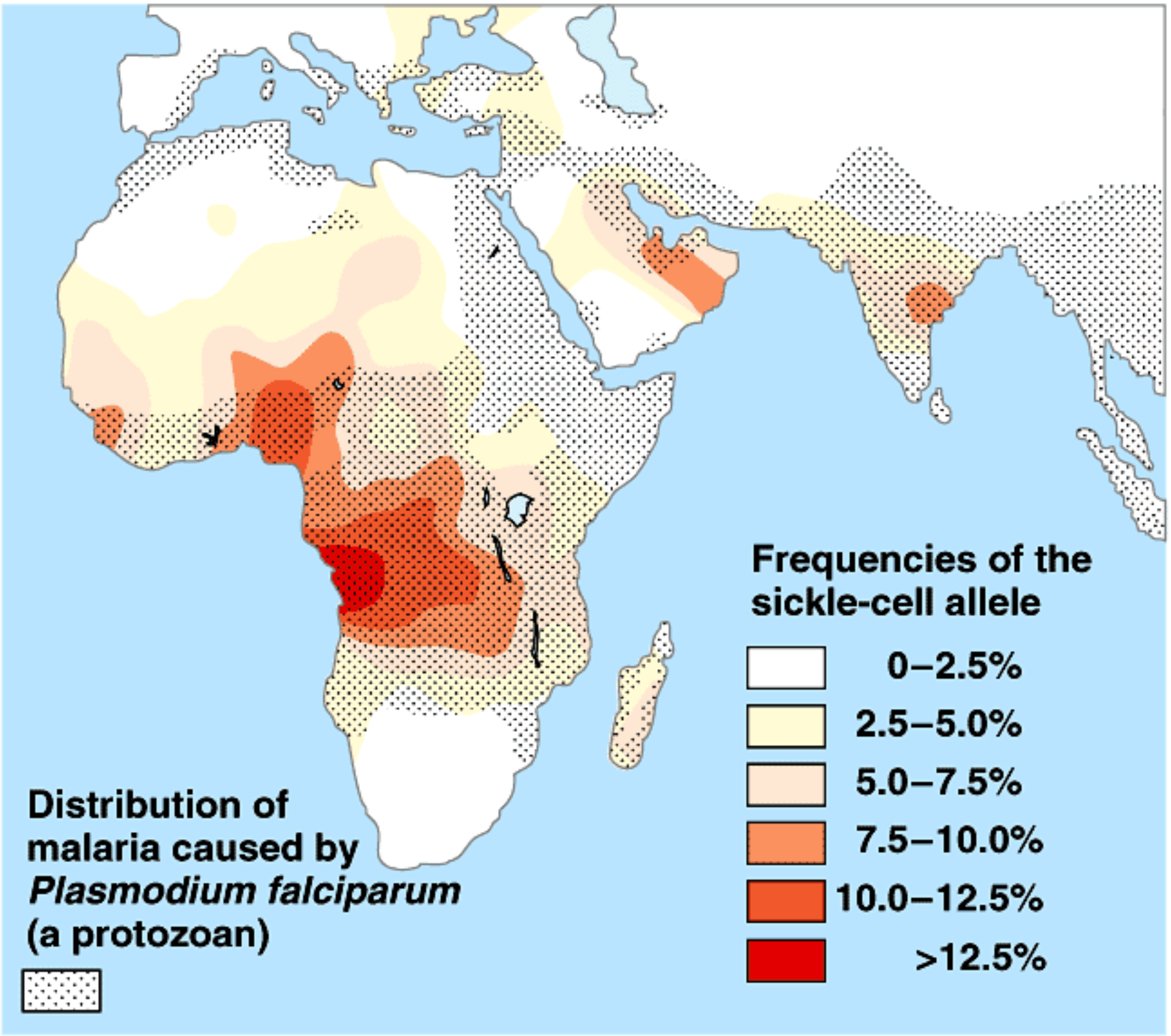


The parental male is the big fish in this picture and the sneaker male is the small fish. https://blog.nationalgeographic.org/2009/06/16/round-goby-fish-have-two-kinds-of-males-scientists-discover/

Balancing selection

- Maintains genetic diversity
- Balanced polymorphism
  - ❑Two or more alleles are kept in balance, and therefore are maintained in a population over the course of many generations
  - ❑Also known as **heterozygote advantage** (sickle cell anemia allele)

Mapping malaria and the sickle-cell allele


Frequencies of the sickle-cell allele
0–2.5%
2.5–5.0%
5.0–7.5%
7.5–10.0%
10.0–12.5%
>12.5%
Distribution of malaria caused by *Plasmodium falciparum* (a protozoan)

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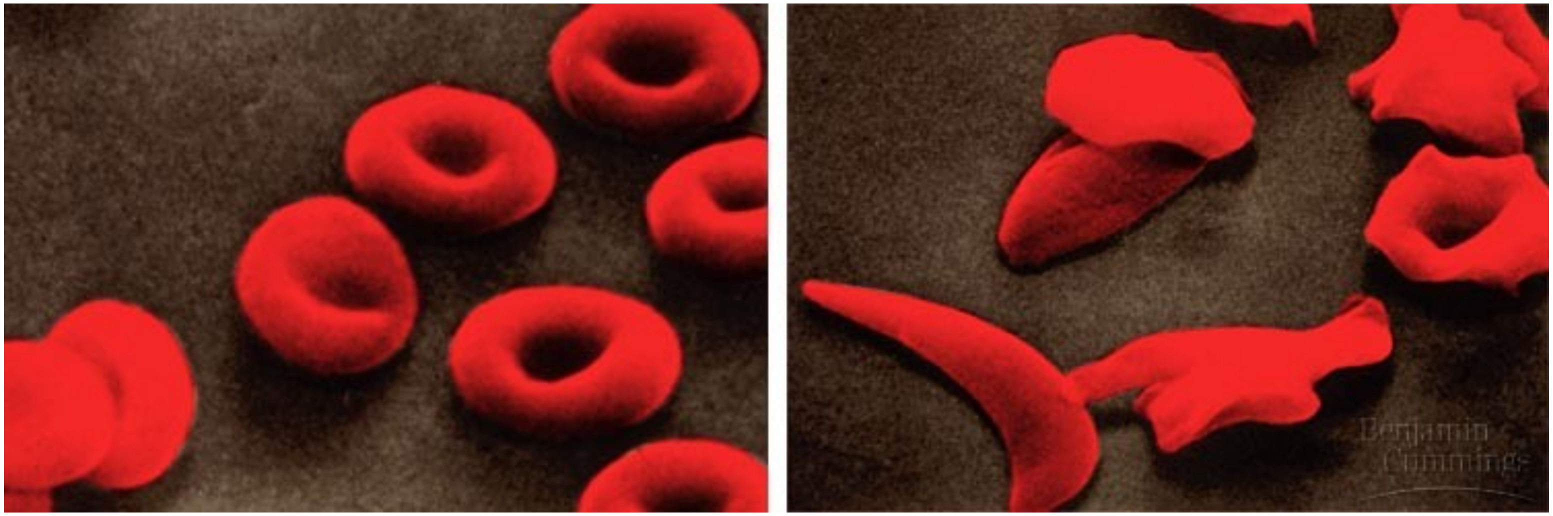
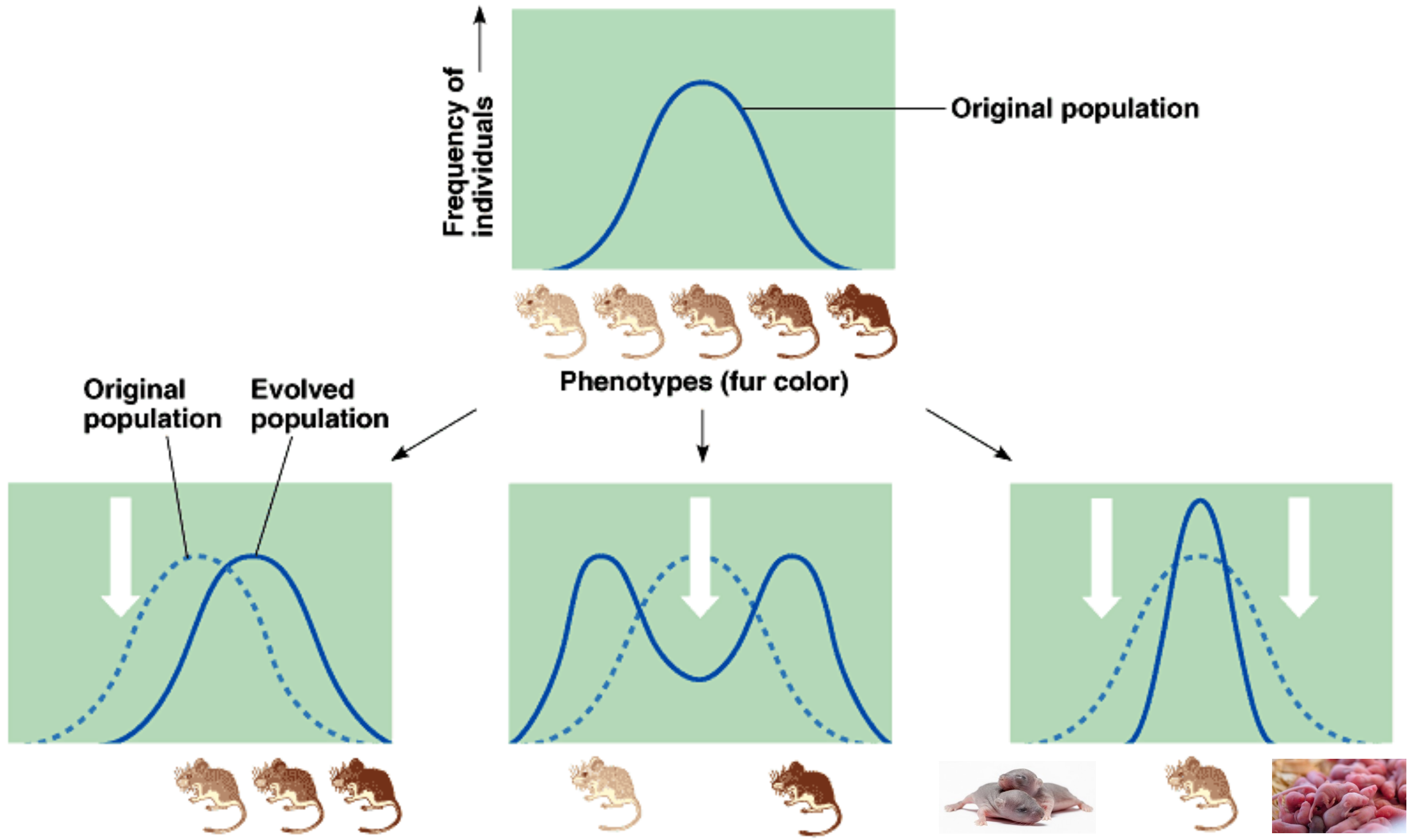
Normal and sickled erythrocytes (red blood cells)



Modes of selection – summary so far



(a) Directional selection

(b) Diversifying selection

(c) Stabilizing selection

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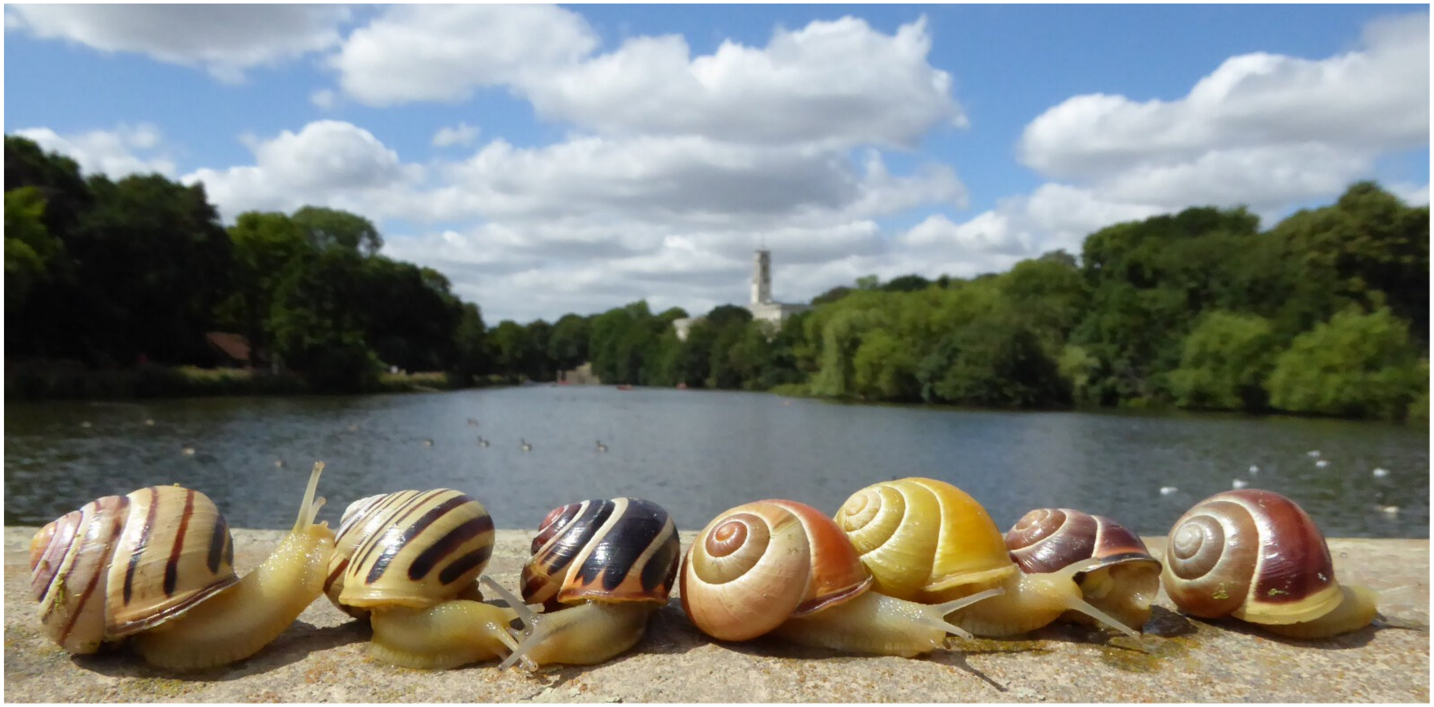
Also called
disruptive

Frequency dependent selection – a type of balancing selection

- Side-blotched lizards.
- https://youtu.be/rafdHxBwIbQ (3.25)
- **Frequency-dependent selection** favors phenotypes that are either common (positive frequency-dependent selection) or rare (negative frequency-dependent selection).
- Males play a game of rock-paper-scissors. Orange a big bully. Blue a steady mating partner. Yellow small and sneaky. Female choice prefers least common color.

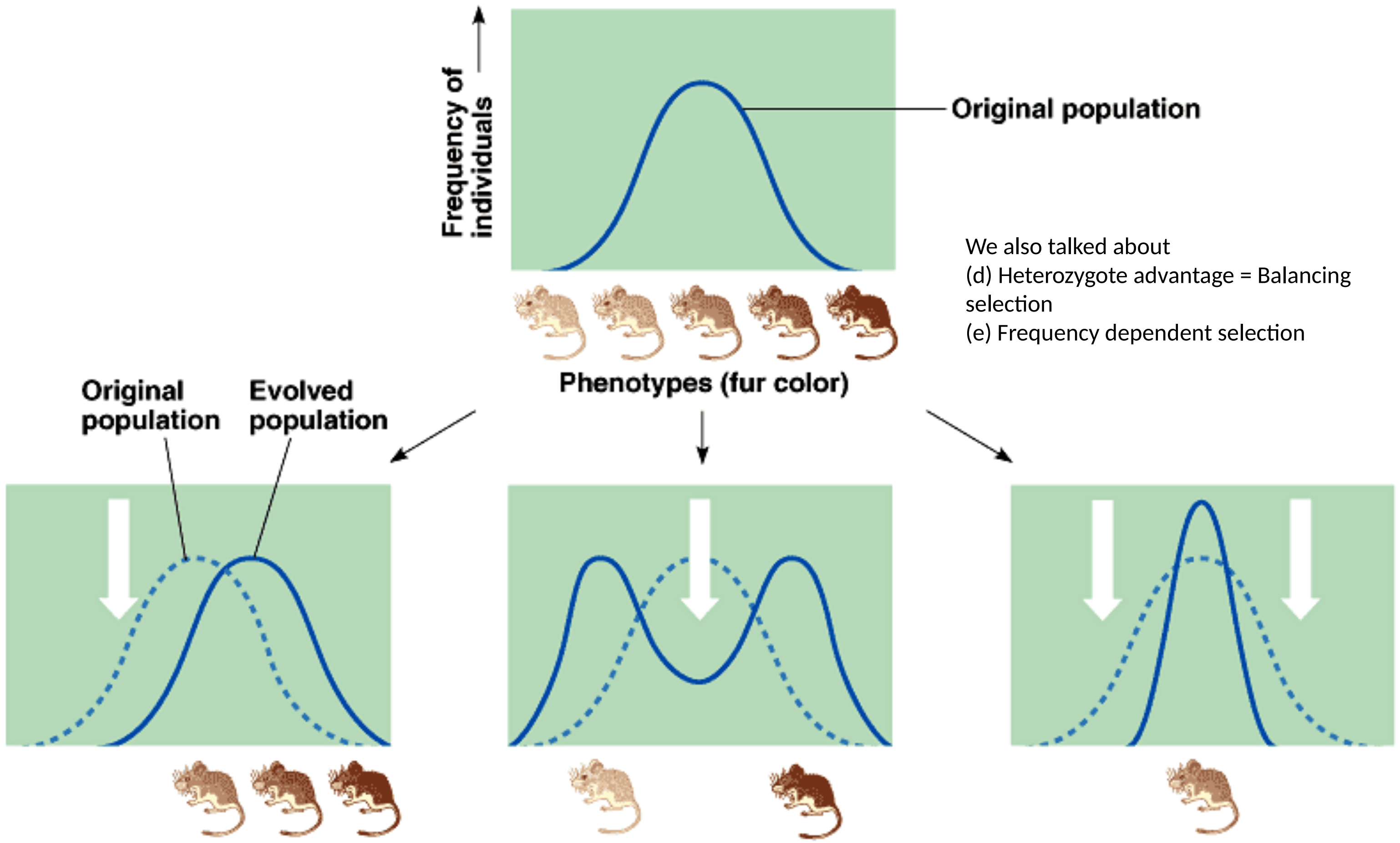
Side blotched lizards

Cepaea nemoralis: *an* example of negative frequency dependent selection



https://phys.org/news/2019-02-humans-struggle-snail-shell-technology.html

Modes of selection - summary



(a) Directional selection

(b) Diversifying selection

(c) Stabilizing selection

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Also called
disruptive

We also talked about
(d) Heterozygote advantage = Balancing selection
(e) Frequency dependent selection

Sexual Selection (non-random mating)

- Form of natural selection
- Directed at certain traits of sexually reproducing species that make it more likely for individuals to find or choose a mate and/or engage in successful mating
- This could lead to any of the modes of selection we have already discussed (but directional selection occurs when females choose extreme traits.

- **Intrasexual selection**
  - ❑Between members of the same sex
  - ❑Horns in male sheep, antlers in male moose, male fiddler crab enlarged claws
  - ❑Males directly compete for mating opportunities or territories
- **Intersexual selection**
  - ❑Between members of the opposite sex
  - ❑Female choice
  - ❑Often results in showy characteristics for males
  - ❑Cryptic female choice
    - Genital tract or egg selects against genetically related sperm
      - ❑Inhibits inbreeding

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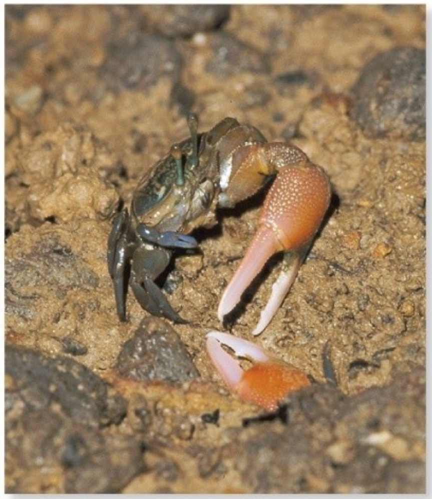
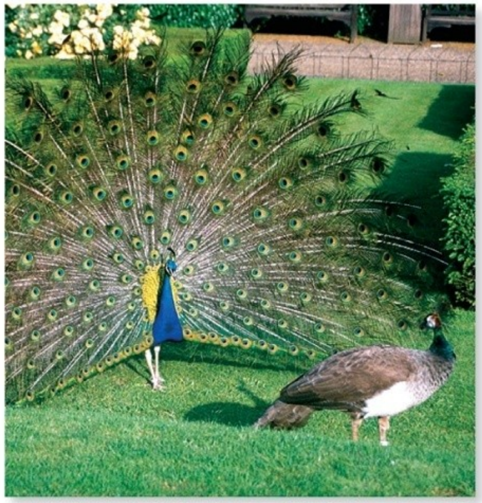
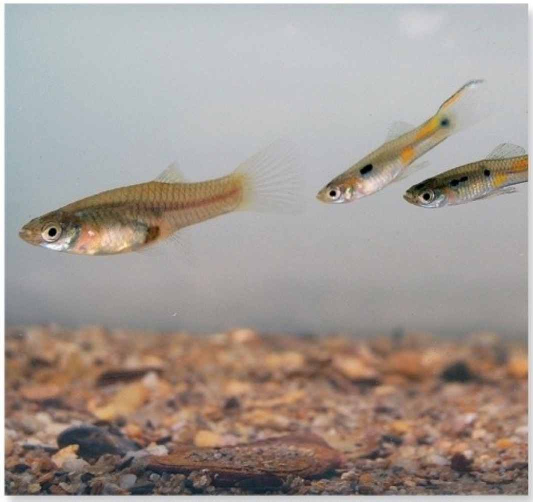


(a) Intrasexual selection



(b) Intersexual selection



(c) Sexual selection balanced by predation

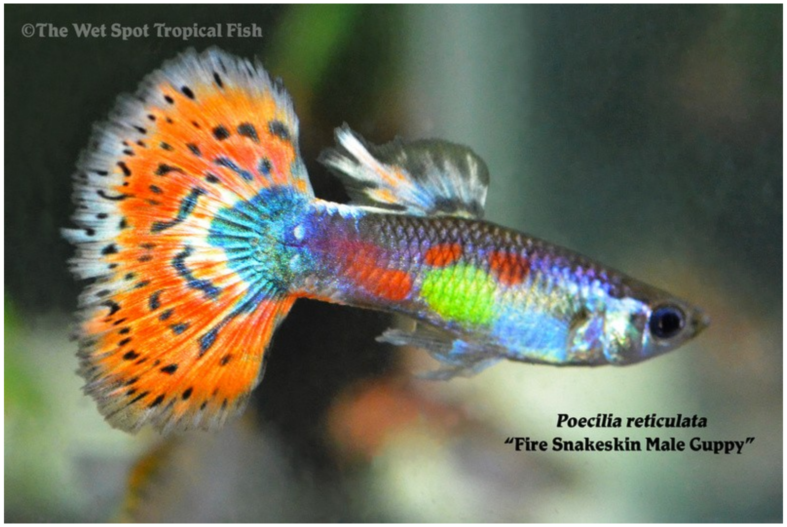
a: © Gerald Cubitt; b: © Topham/The Image Works; c: © Photo by Darren P. Croft, University of Exeter UK

- Mastering Bio Chapter 26 due Saturday, Feb 18
- Midterm 1 opens Friday, Feb 17th on Canvas with Respondus Lockdown Browser. Make sure you have the program.

Respondus Lockdown Browser

- Some instructors may require that you use Respondus when taking online exams or quizzes. Respondus Lockdown Browser is a custom browser that locks down the testing environment within Canvas. When you use the Respondus Lockdown Browser you are unable to print, copy, go to a URL, or access other applications. When an assessment is started, you are locked into it until the exam is submitted for grading. Available for both Windows and Mac.
- Respondus Monitor is a companion product for the Respondus Lockdown Browser that enables institutions to protect the integrity of non-proctored online exams. You use your own computer and a webcam to record assessment sessions, all without leaving Canvas.
- Student Quick Start Guide for Respondus
- Installation for Fresno State Users
  Respondus Lockdown Browser uses a standard Windows or Mac installer that can be downloaded by students from the following link. Please note this link is unique to Fresno State users:
  http://www.respondus.com/lockdown/download.php?id=749643058

- Explains traits that decrease survival but increase reproductive success
- ex: **Guppy, *Poecilia reticulata*** – Male is brightly colored compared to the female
- Females prefer brightly colored males



- In places with **few predators,** the males tend to be brightly colored
- In places where predators are **abundant,** brightly colored males are less plentiful because they are subject to predation
- Relative abundance of brightly and dully colored males depends on the **balance** between sexual selection, which favors bright coloring, and escape from predation, which favors dull coloring. Cost benefit approach.

Widowbirds

Genetic Drift

- Changes allelic frequency due to **random chance (random sampling)**
- Random events **unrelated to fitness**
- The allele is generally either **lost** or **fixed**
- Frequency reaches 0% or 100%
- Faster in smaller populations

Bottleneck (1 type of genetic drift)

- Population reduced dramatically and then rebuilds
- Randomly eliminates members without regard to genotype
- Surviving members may have allele frequencies different from original population
- Allele frequencies can drift substantially when population is small
- New population likely to have **less genetic variation**
- “In one fell swoop, the genetic structure of the survivors becomes the genetic structure of the entire population, which may be very different from the pre-disaster population.” Openstax

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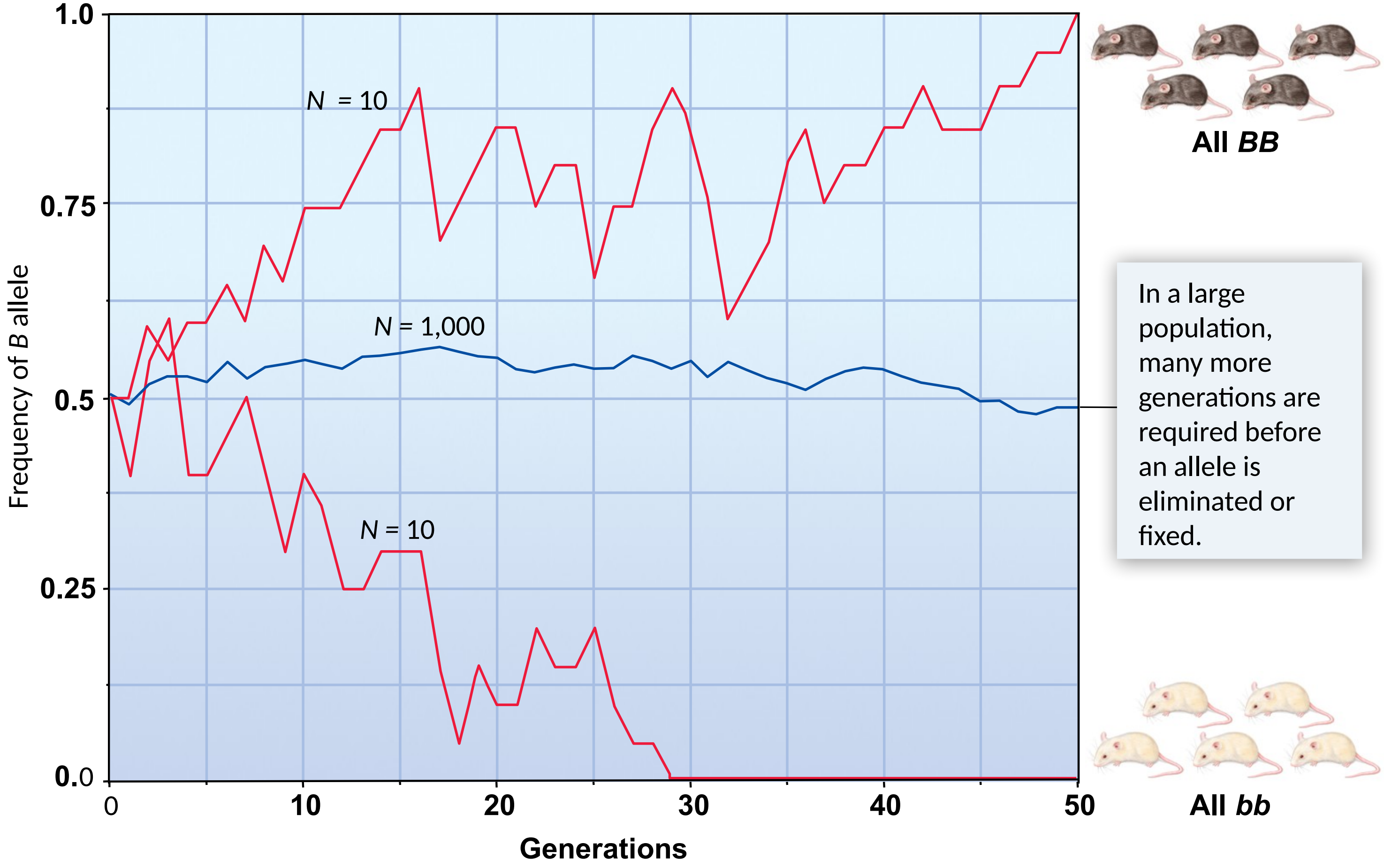
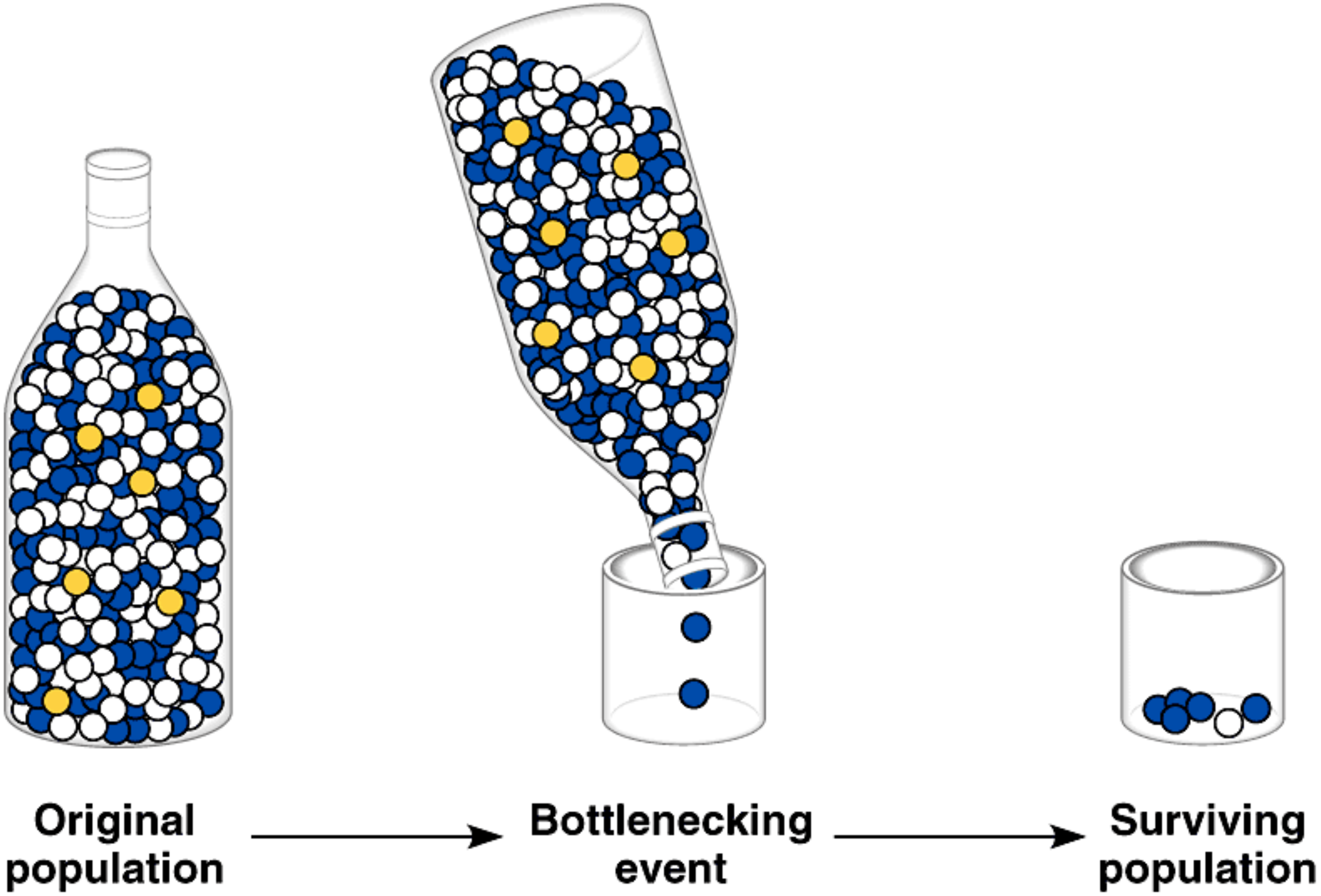


In a large population, many more generations are required before an allele is eliminated or fixed.

The bottleneck effect



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Cheetahs, the bottleneck effect (10,000 years ago – end of ice age, plus poaching and habitat loss.)

http://evolution.berkeley.edu/evolibrary/news/070701_cheetah

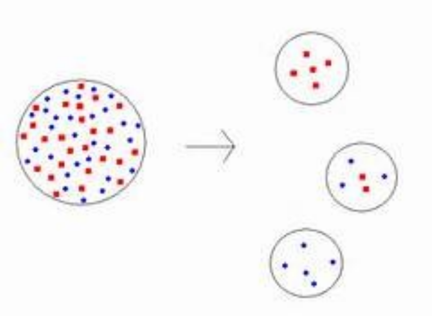
Addo elephants of South Africa

Addo elephants

- Originally a large population with an uncommon allele for reduced or absent tusks in females only.
- Population reduced to 11 individuals by 1930, after a power hunter was contracted to kill all the local population by farmers. This was composed of 8 females and 3 males.
- Park established to protect remaining elephants.
- Population is now up to 324, all due to reproduction, no immigration.

Founder effect (another type of genetic drift)

- Small group of individuals separates from a larger population and establishes a **new population**
- Relatively small founding population expected to have less genetic variation than original population
- Allele frequencies in founding population may differ markedly from original population
- Similar consequences to a bottleneck
- Darwin's finches blown over to the Galapagos
- Canadian goose/Hawaiian goose



Migration and Nonrandom Mating

- **Gene flow** occurs when individuals migrate between populations having different allele frequencies
- Migration tends to **reduce differences** in allele frequencies between the two populations
- Tends to enhance genetic diversity within a population

Gene flow and human evolution

SPECIAL ISSUE
TIME
Take a good look at this woman. She was created by a computer from a mix of several races. What you see is a remarkable preview of . . .
THE NEW FACE OF AMERICA
How Immigrants Are Shaping the World's First Multicultural Society
Benjamin Cummings

- **Gene flow** tends to reduce differences between populations
- Gene flow is accelerated with increases in migration rates
- May lead to population coalescence

Nonrandom mating

- One of the conditions required to establish the Hardy-Weinberg equilibrium is **random mating**
  - ❑Individuals choose their mates irrespective of their genotypes and phenotypes
- Forms of nonrandom mating
  - ❑**Assortative / disassortative mating**
  - ❑**Inbreeding**

- **Assortative mating (homogamy)**
  - ❑Individuals with similar phenotypes are more likely to mate (color, body size, human royals)
  - ❑Increases the proportion of homozygotes
- **Disassortative mating (heterogamy)**
  - ❑Dissimilar phenotypes mate preferentially
  - ❑Favors heterozygosity (maintains variation)

- **Inbreeding**
  - Choice of mate based on genetic history
  - Does not favor any particular allele but does increase the likelihood the individual will be homozygous
  - May have negative consequences with regard to recessive alleles
  - Lower mean fitness of a population if homozygous offspring have a lower fitness value
  - INBREEDING DEPRESSION

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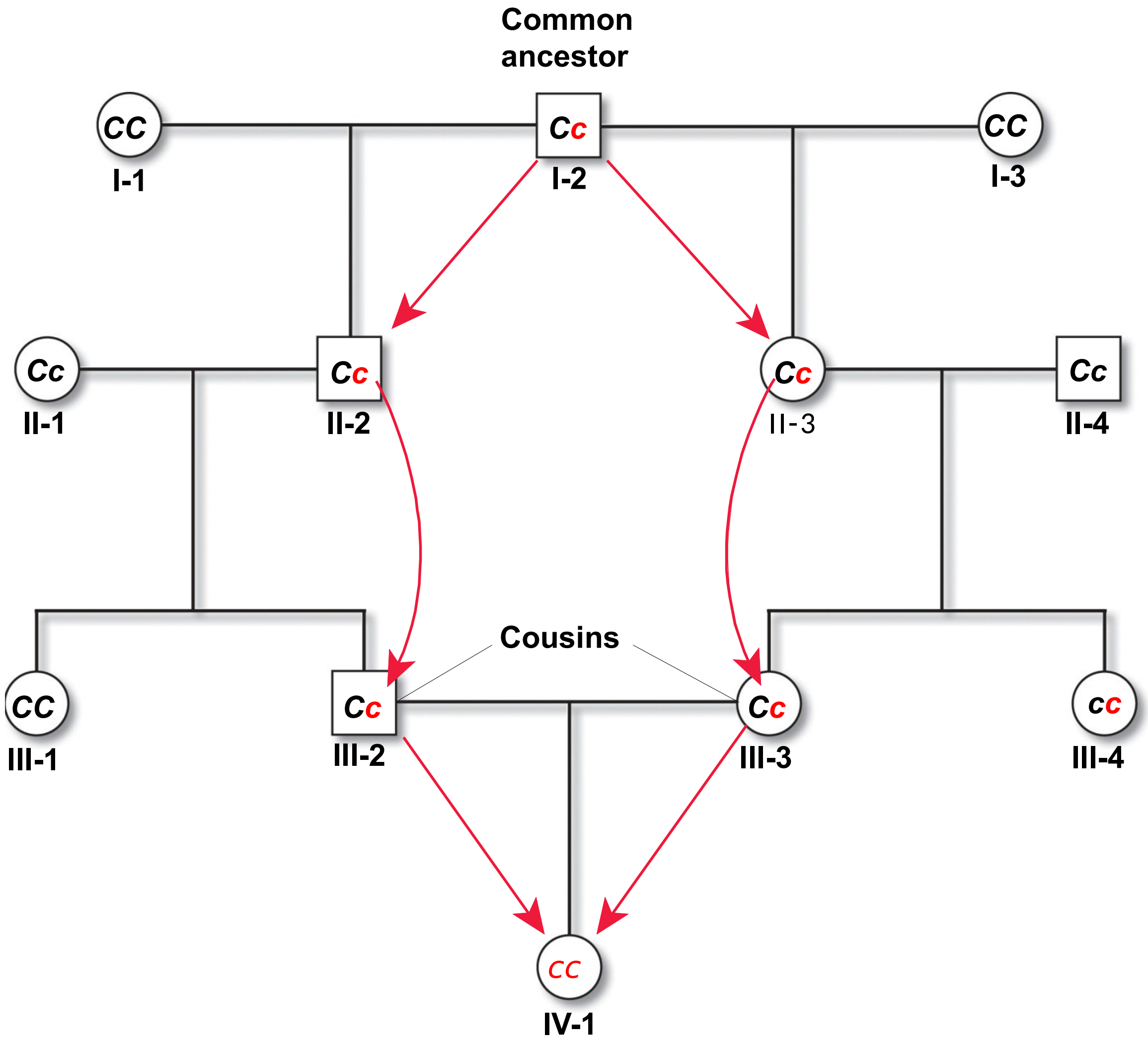


If 36% of an African population is born with a severe form of sickle-cell anemia (ss), what percentage of the population will be more resistant to malaria because they are heterozygous(Ss) for the sickle-cell gene?
(Would you have the same numbers if the problem said 36 individuals out of 205?)
(Would you have the same numbers if the problem said 36% of a population of 45,000 people?)

Show your work. You are solving for Genotype frequency of the heterozygote.

0.36 genotype frequency

Allele frequency (s) = square root of 0.36 = 0.6 =q

p+q=1. p=0.4

2pq = 2x0.4x0.6 = 0.48

SS frequency = 0.16

0.16 + 0.48 + 0.36 = 1

Phylogeny and Systematics

Key Topics:

- **Phylogenetic Trees**
- **Taxonomy, Classification and Systematics**
- **Cladistics**
- **Molecular Clocks**
- **Horizontal Gene Transfer**

Phylogenetic Trees

- **Phylogeny** – evolutionary history of an organism or group of organisms
- To propose a phylogeny, biologists use the tools of **systematics**
- Trees are usually based on morphological or genetic data or both.
- The goal of systematics and taxonomy is to name organisms according to their evolutionary relationships.

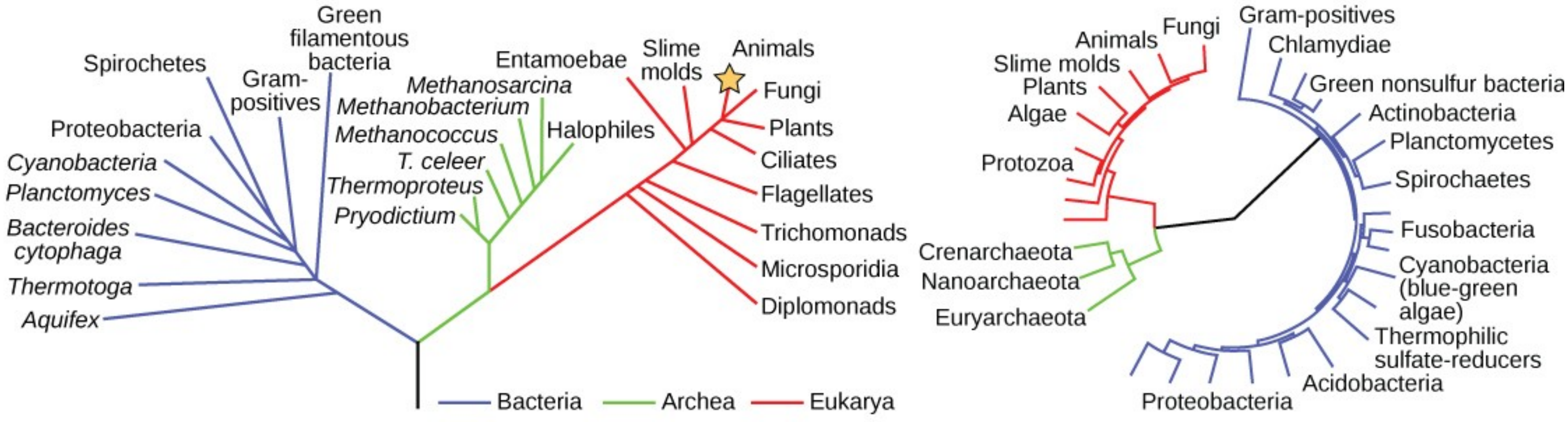
Phylogenetic tree

- Diagram that describes phylogeny, evolutionary pathways and connections among organisms.
- A phylogenetic tree is an **hypothesis** of evolutionary relationships among various species

Rooted and unrooted trees

- If the phylogenetic tree has a single lineage at the base representing a common ancestor to everything on the tree, it is called “rooted”.
- An unrooted tree doesn’t show the common ancestor, but still shows relationships among species

Figure 20.2



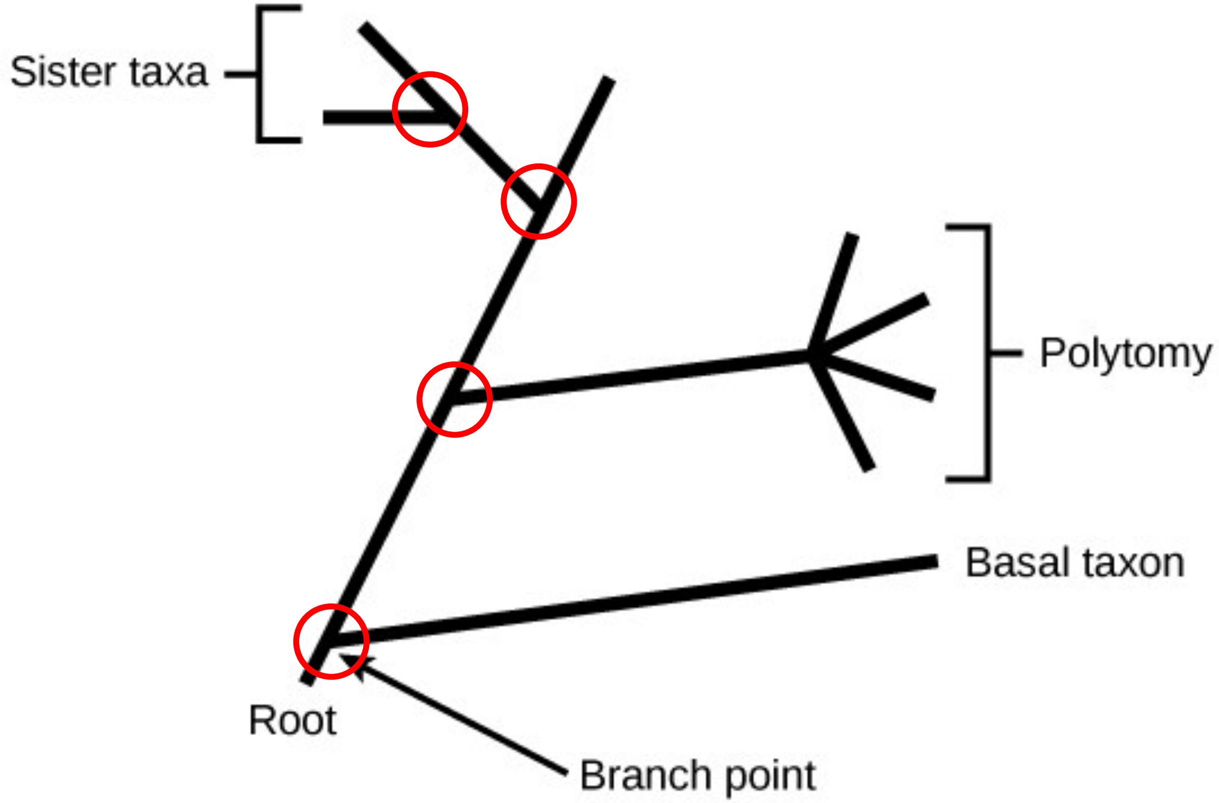
(a) Rooted phylogenetic tree

(b) Unrooted phylogenetic tree

- Both of these phylogenetic trees shows the relationship of the three domains of life—Bacteria, Archaea, and Eukarya—but the (a) rooted tree attempts to identify when various species diverged from a common ancestor (recent common ancestor) while the (b) unrooted tree does not (general relatedness). (credit a: modification of work by Eric Gaba)

- Branch point = point where a split occurs
- Basal taxon = lineage splitting off early from the root remaining unbranched
- Sister taxa = 2 lineages stem from same branch point
- Polytomy = branch with more than 2 lineages (still working out the relationships)

Figure 20.3



- The root of a phylogenetic tree indicates that an ancestral lineage gave rise to all organisms on the tree. A branch point indicates where two lineages diverged. A lineage that evolved early and remains unbranched is a basal taxon. When two lineages stem from the same branch point, they are sister taxa. A branch with more than two lineages is a polytomy.

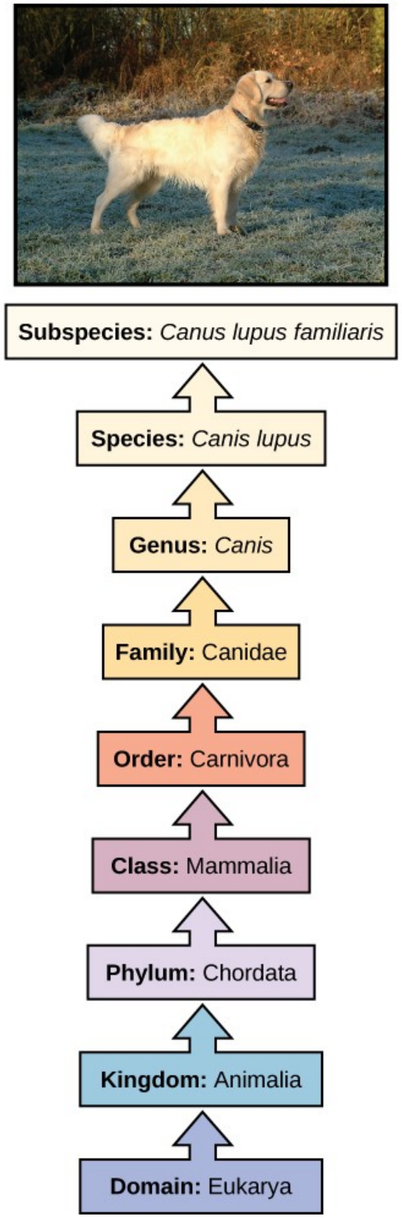
Taxonomy

- **Taxonomy**
  - Science of describing, naming, and **classifying** living and extinct organisms (and viruses)
- **Systematics**
  - Study of biological diversity and the evolutionary relationships among organisms, both extinct and modern
- Taxonomic groups are based on hypotheses regarding evolutionary relationships derived from systematics

Taxonomy

- Hierarchical system involving successive levels
- Each group at any level is called a **TAXON** (plural **TAXA**)
- Broadest (most inclusive) level is **Domain**
  - All of life belongs to one of 3 domains
  - **Bacteria, Archaea,** and **Eukarya (Eukaryota)**
  - Other **taxa** include Kingdom, Phylum, Class, Order, Family, *Genus* and *species*

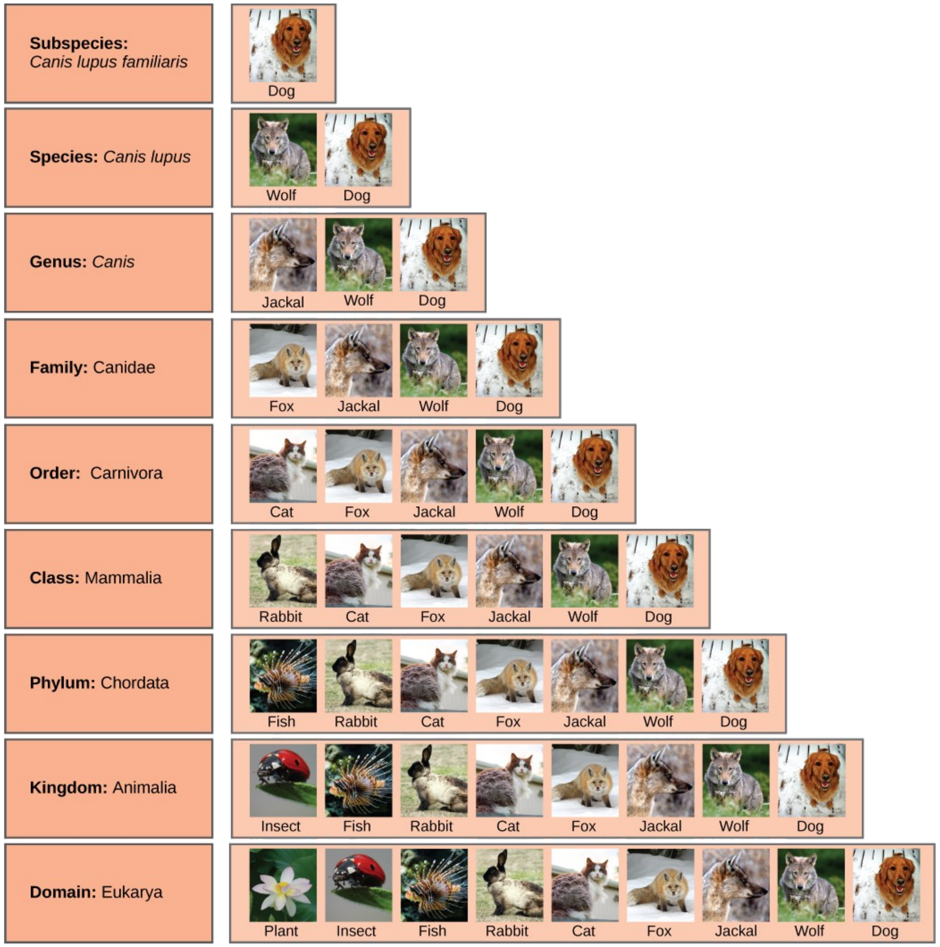
Figure 20.5

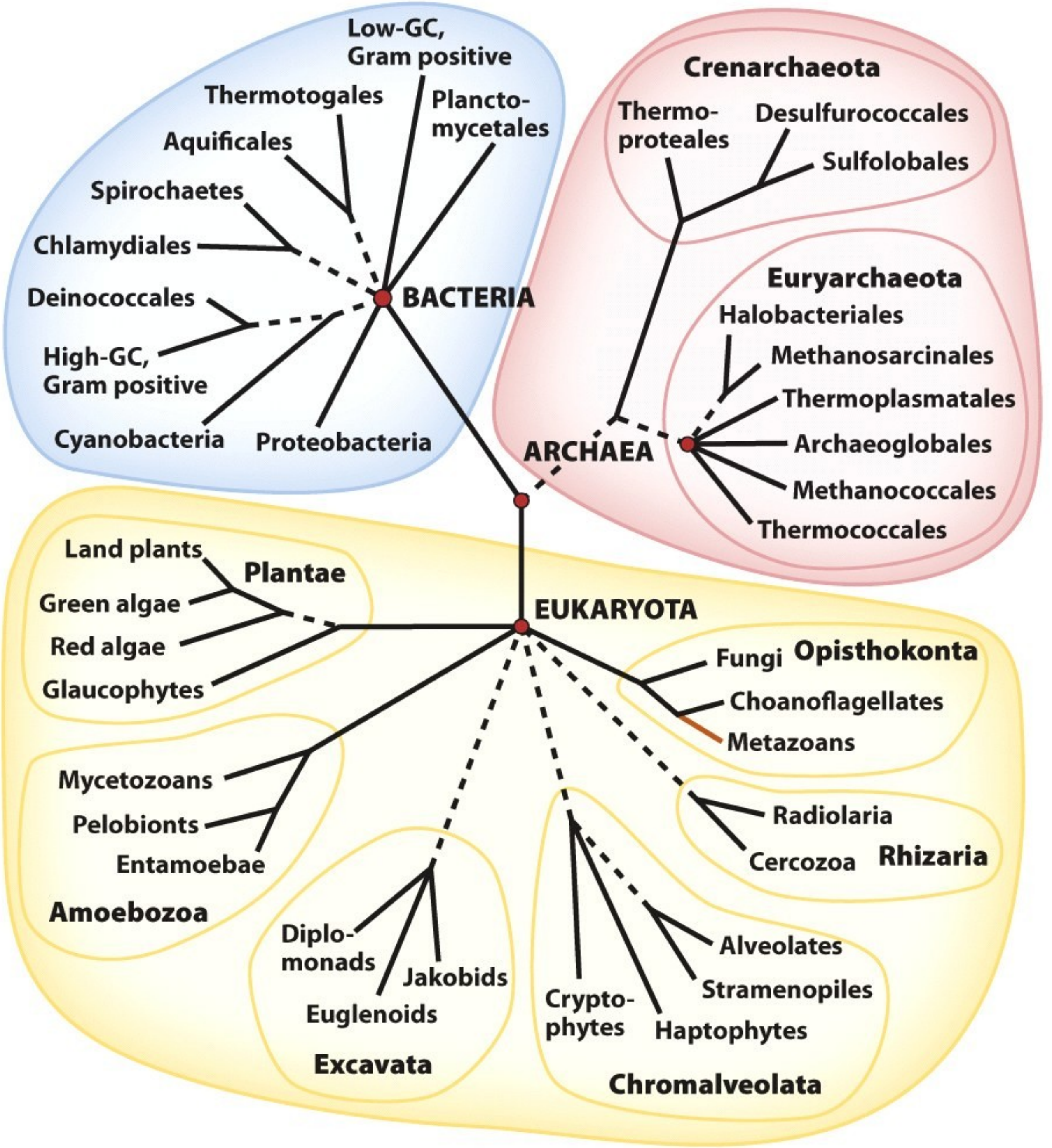


- The taxonomic classification system uses a hierarchical model to organize living organisms into increasingly specific categories. The common dog, *Canis lupus familiaris*, is a subspecies of *Canis lupus*, which also includes the wolf and dingo. (credit “dog”: modification of work by Janneke Vreugdenhil)

Figure 20.6

- At each sublevel in the taxonomic classification system, organisms become more similar. Dogs and wolves are the same species because they can breed and produce viable offspring, but they are different enough to be classified as different subspecies. (credit “plant”: modification of work by “berduchwal”/Flickr; credit “insect”: modification of work by Jon Sullivan; credit “fish”: modification of work by Christian Mehlführer; credit “rabbit”: modification of work by Aidan Wojtas; credit “cat”: modification of work by Jonathan Lidbeck; credit “fox”: modification of work by Kevin Bacher, NPS; credit “jackal”: modification of work by Thomas A. Hermann, NBII, USGS; credit “wolf”: modification of work by Robert Dewar; credit “dog”: modification of work by “digital_image_fan”/Flickr)


Subspecies: *Canis lupus familiaris*
Dog
Species: *Canis lupus*
Wolf Dog
Genus: *Canis*
Jackal Wolf Dog
Family: Canidae
Fox Jackal Wolf Dog
Order: Carnivora
Cat Fox Jackal Wolf Dog
Class: Mammalia
Rabbit Cat Fox Jackal Wolf Dog
Phylum: Chordata
Fish Rabbit Cat Fox Jackal Wolf Dog
Kingdom: Animalia
Insect Fish Rabbit Cat Fox Jackal Wolf Dog
Domain: Eukarya
Plant Insect Fish Rabbit Cat Fox Jackal Wolf Dog



Evolution, 1/e Figure 4.2a

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Supergroups are circled.

Eukaryotic Supergroups

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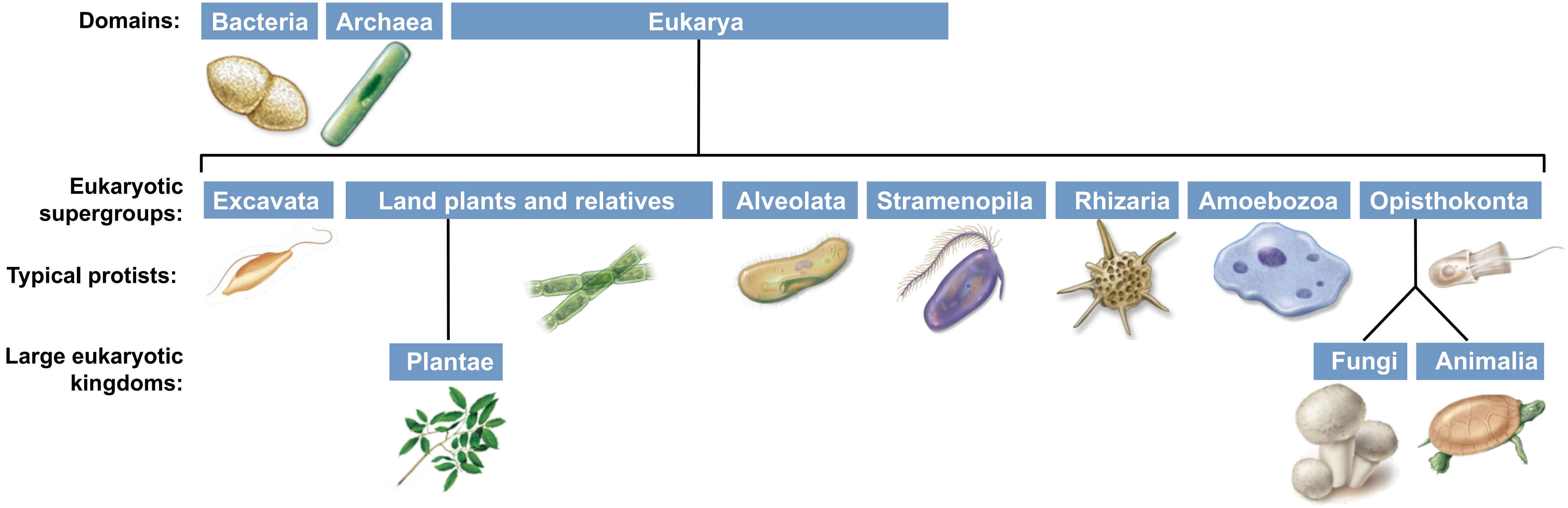

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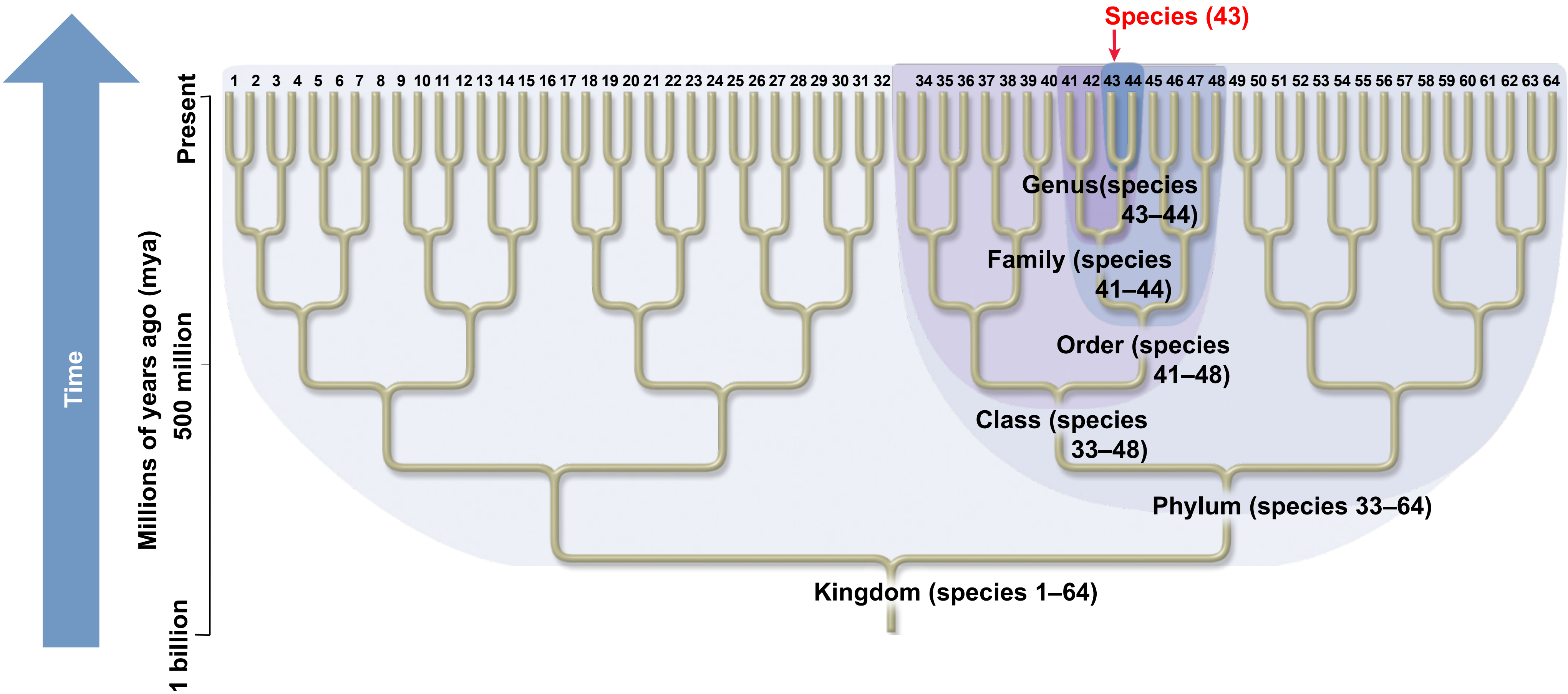


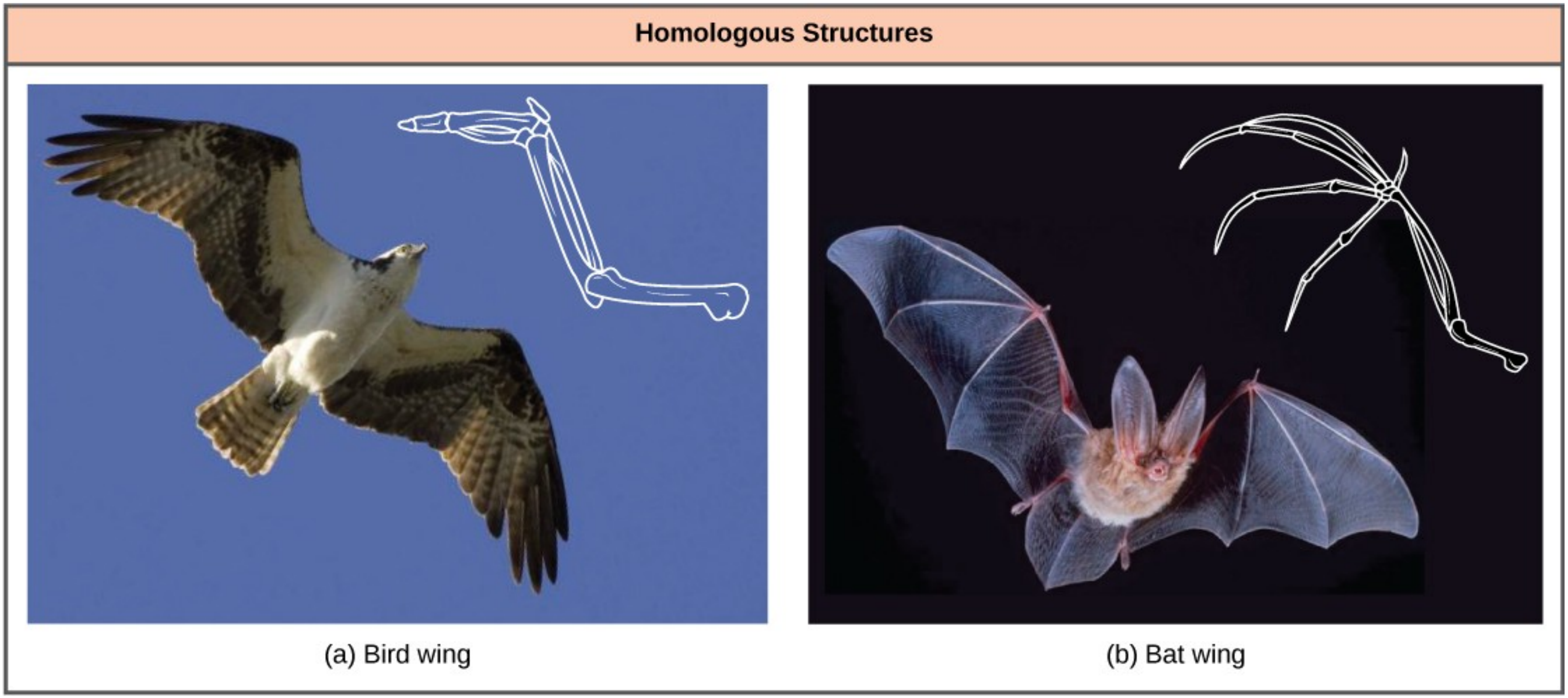
Binomial nomenclature (Linnaeus)

- ***E.g. Homo sapiens*, Canis lupus**
- Genus name always Capitalized
- species never capitalized
- Both names either *italicized* or underlined (not both)
- *Canis lupus familiaris* adds subspecies

Homology

- Similarities among various species that occur because they are derived from a **common ancestor**
- E.g. Bat wing, human arm and cat front leg
- Genes can also be homologous if they are **derived** (changed) from the **same ancestral gene**

Figure 20.7

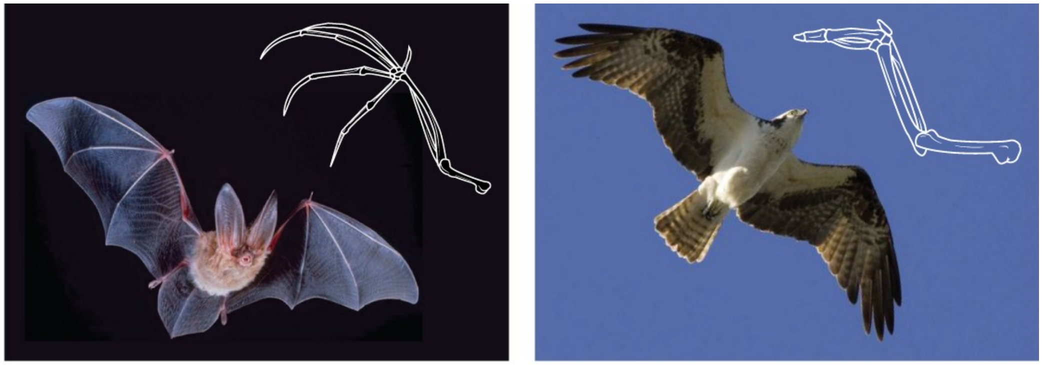


- Bat and bird wings are homologous structures, indicating that bats and birds share a common evolutionary past. (credit a: modification of work by Steve Hillebrand, USFWS; credit b: modification of work by U.S. DOI BLM)
- Homologous as arms or limbs, from common tetrapod ancestor
- (Flight is NOT homologous, because they didn’t have a common ancestor that flew)

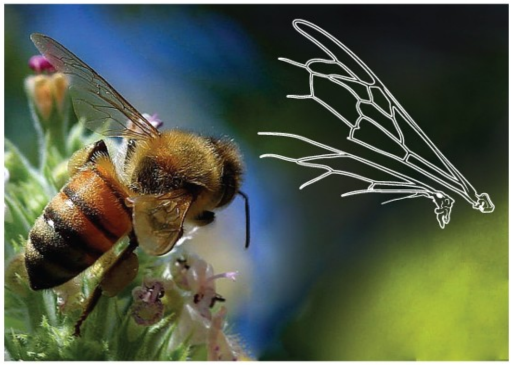
Morphological analysis

- First systematic studies focused on **morphological features** of extinct and modern species
- **Convergent evolution** - why is this a problem for systematic studies based on morphological features?

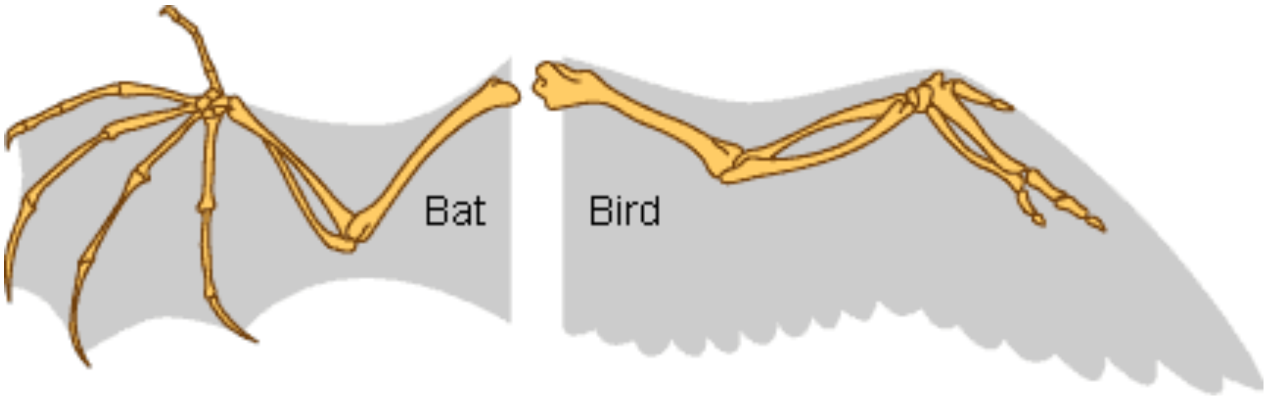
Figure 20.8

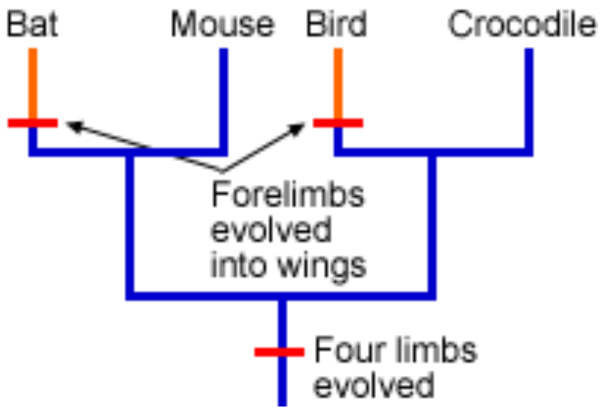

(a) Bat wing

(b) Bird wing


(c) Insect wing

- The (c) wing of a honeybee is similar in shape to a (b) bird wing and (a) bat wing, and it serves the same function. However, the honeybee wing is not composed of bones and has a distinctly different structure and embryonic origin. These wing types (insect versus bat and bird) illustrate an analogy—similar structures that do not share an evolutionary history. (credit a: modification of work by Steve Hillebrand, USFWS; credit b: modification of work by U.S. DOI BLM; credit c: modification of work by Jon Sullivan)
- An analogy (or homoplasy) is a characteristic shared with another organism because of similar environmental constraints through natural selection, but with separate evolutionary origins. (Convergent evolution)





Bird and bat wings are HOMOLOGOUS as front limbs, but are ANALOGOUS as wings. Why?

Images from University of California Museum of Paleontology's Understanding Evolution (http://evolution.berkeley.edu).

Molecular systematics

- Analysis of genetic data, such as DNA and amino acid sequences, to identify and study genetic homologies and test phylogenetic hypotheses
- DNA and amino acid sequences from closely related species are more similar to each other than to sequences from more distantly related species
- Taxonomy, Phylogeny, Systematics, Cladistics

Cladistics – Building a phylogenetic tree

- **Cladistics**: System of classification of species based on evolutionary relationships

- Groups of organisms descended from a single ancestor are sorted into **clades**. Choose the tree that requires the **least complex explanation. (Parsimony) = a hypothesis of relationships that requires the smallest number of character changes (smallest # of DNA mutations) is most likely to be correct**.

- Phylogenetic trees = **cladograms**

- **Monophyletic group** or **clade**
  - Group of species consisting of the most recent common ancestor and **all of its descendants**
- Smaller and more recent clades are nested within larger clades that have older common ancestors
- **Paraphyletic group**
  - Contains a common ancestor and some, but not all, of its descendants
- **Polyphyletic group**
  - Contains more than one ancestor and their descendants
- If it is found that a named group of organisms is either para or polyphyletic, then the taxonomy is revised.

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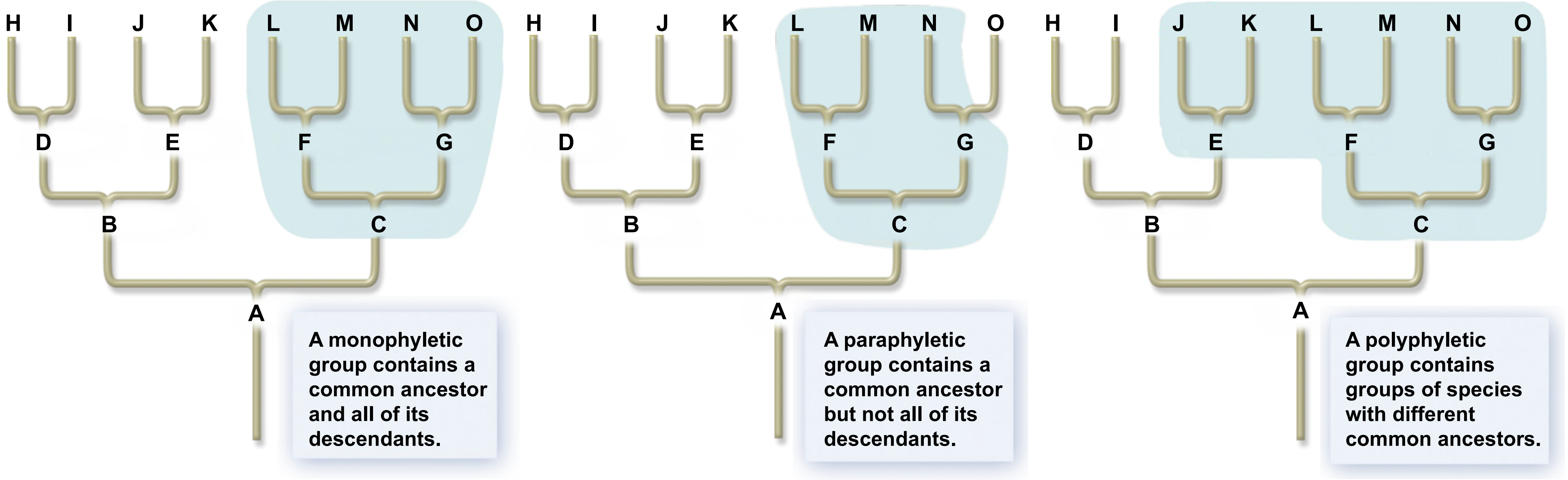

A monophyletic group contains a common ancestor and all of its descendants.

A paraphyletic group contains a common ancestor but not all of its descendants.

A polyphyletic group contains groups of species with different common ancestors.

(a) Monophyletic group

(b) Paraphyletic group

(c) Polyphyletic group

- Over time, taxonomic groups will be reorganized so only monophyletic groups are recognized

- **Reptiles** were a paraphyletic group because birds were excluded

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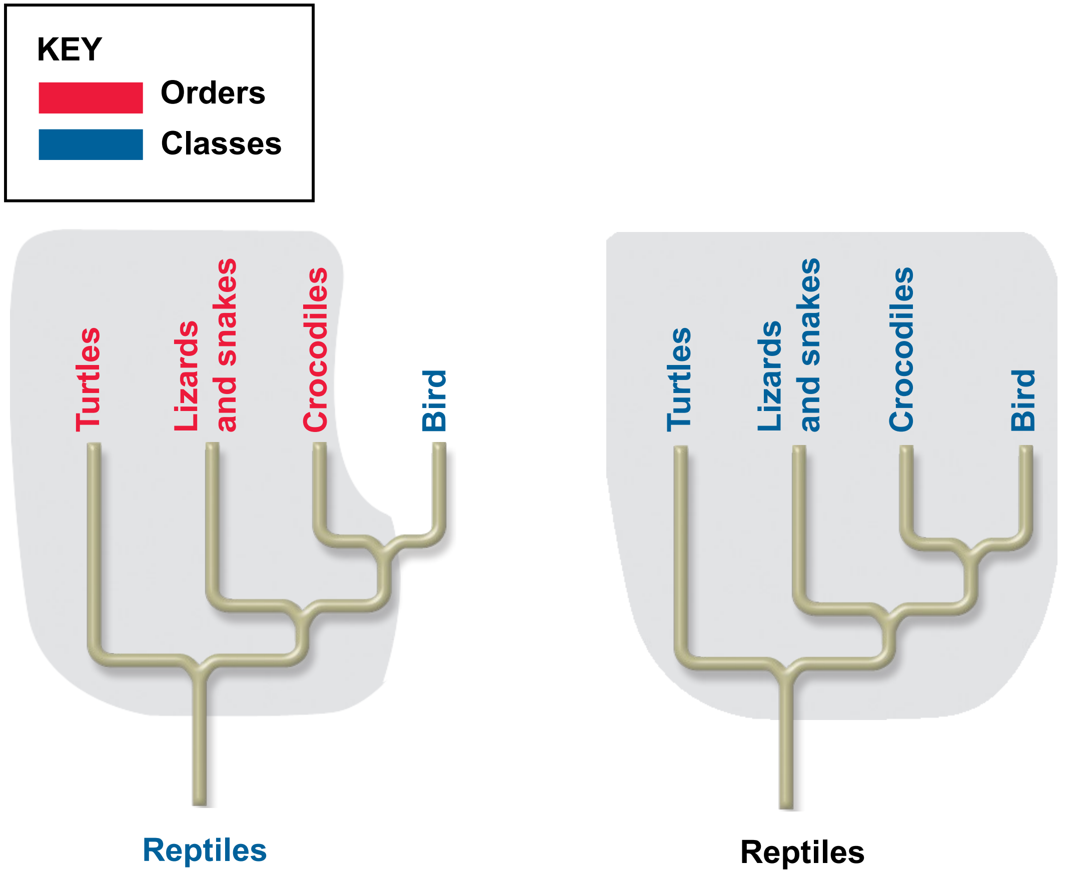

(a) Reptiles as a paraphyletic taxon

(b) Reptiles as a monophyletic taxon

FEATURE INVESTIGATION

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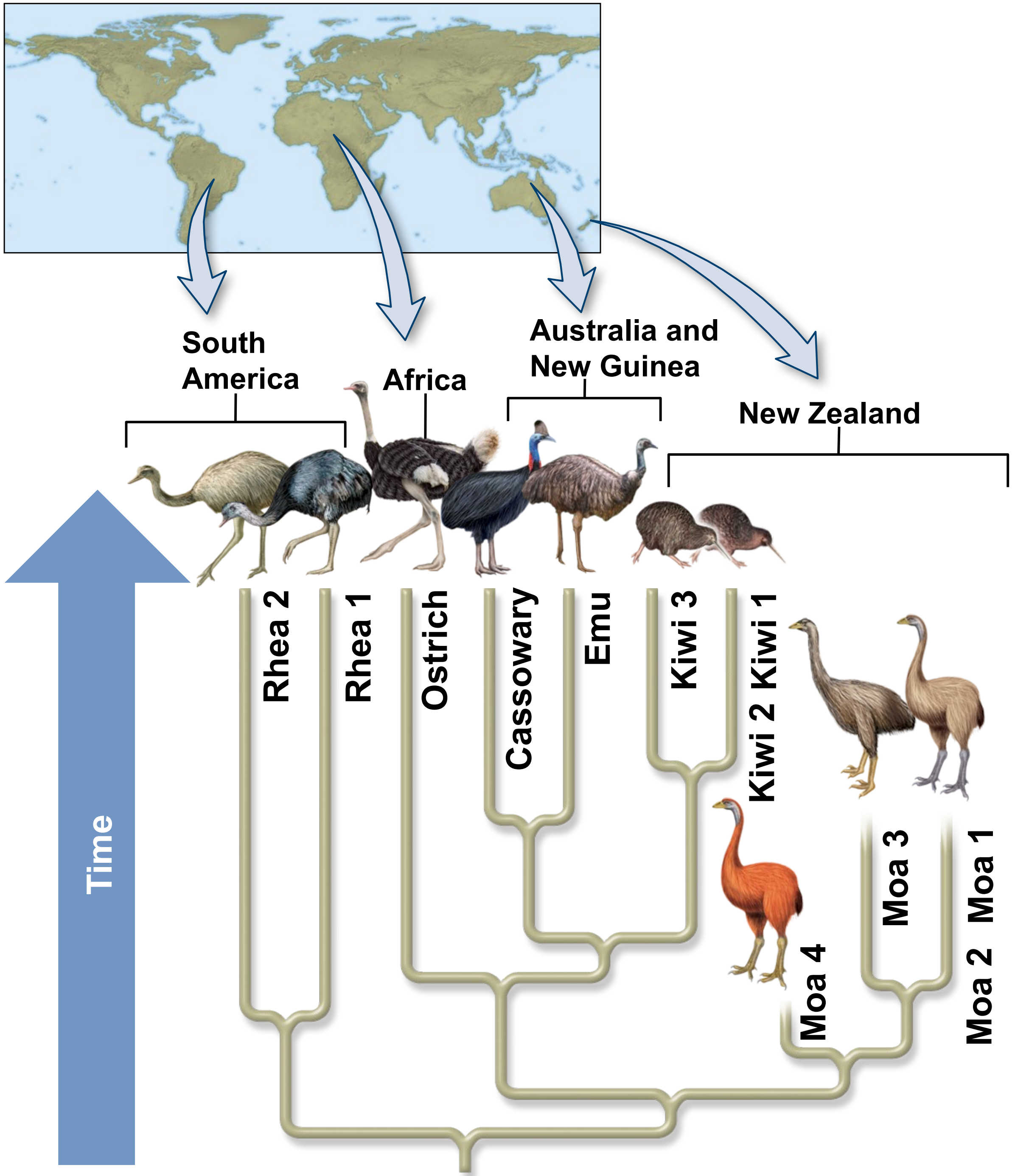


KIWI

Kiwi

- Cladistic approach compares homologous traits, also called **characters,** which may exist in two or more character states

- Shared ancestral trait (Plesiomorphy).
  - An evolutionary trait that is homologous within a particular group of organisms but is not unique to members of that group. For example, vertebrae are found in zebras, cheetahs, orangutans and lizards, but the common ancestor in which this trait first evolved is so distant that the trait is shared by many other animals. Therefore, possession of vertebrae sheds no light on the phylogenetic relations of the 3 mammal species.
  - Characteristic found in ancestor to the group, and all organisms in the clade have that trait. Inherited from ancestors **older** than their last common ancestor

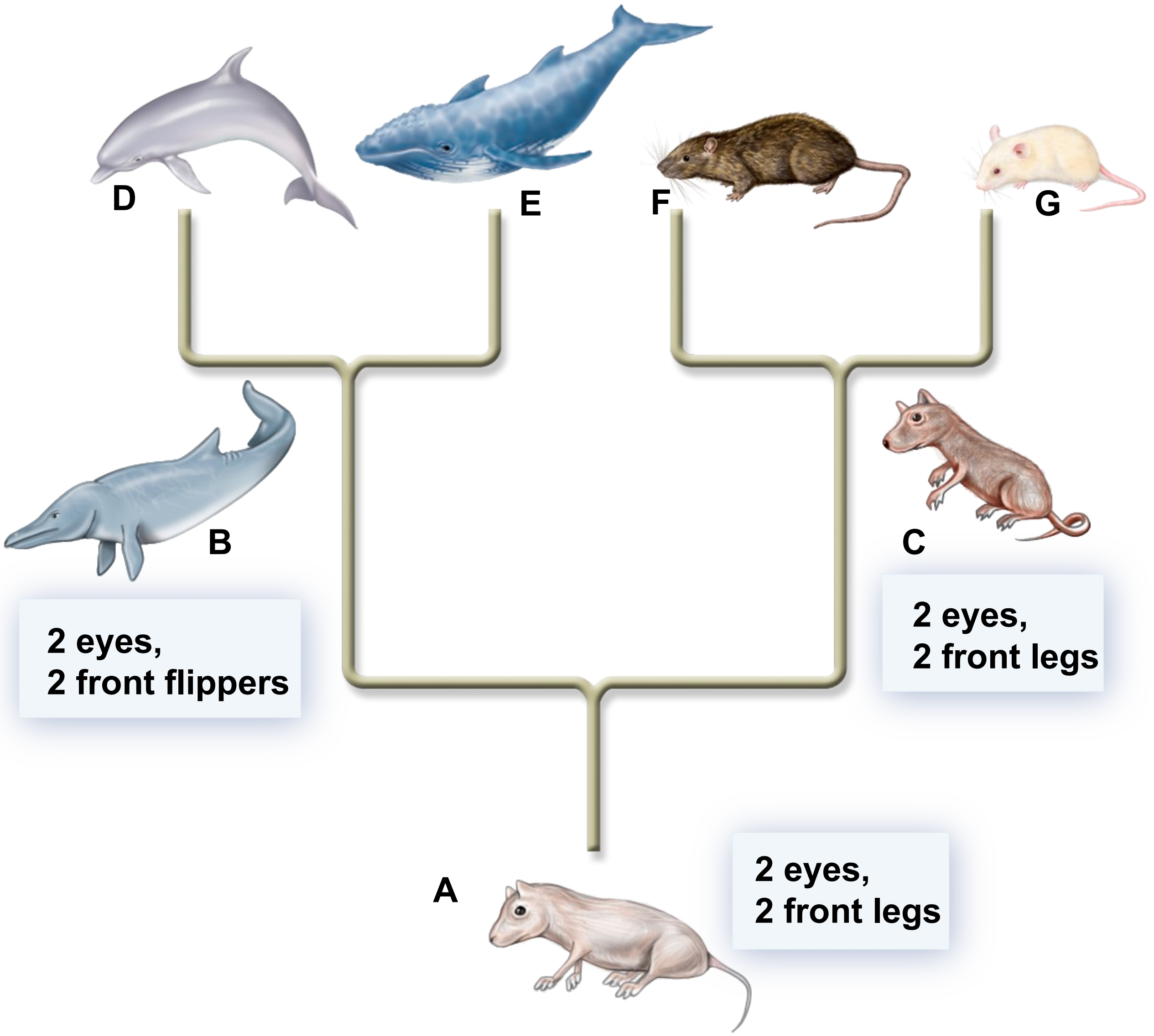
Shared derived character (Synapomorphy)

  - Shared by two or more species or taxa and has originated in their most recent common ancestor
  - A novel evolutionary trait that is unique to a particular species and all its descendants and which can be used as a defining character for a species or group in phylogenetic terms. The possession of feathers is unique to birds and defines all members of the clade Aves.
- Basis of the cladistic approach is to analyze many shared derived characters to discover the pathway that gave rise to those species (ex. Milk in mammals compared to mammals as tetrapods)

With regard to species D and E,

1. Shared ancestral (primitive) character(s) ________

A. Eyes
B. Flippers
C. Backbone

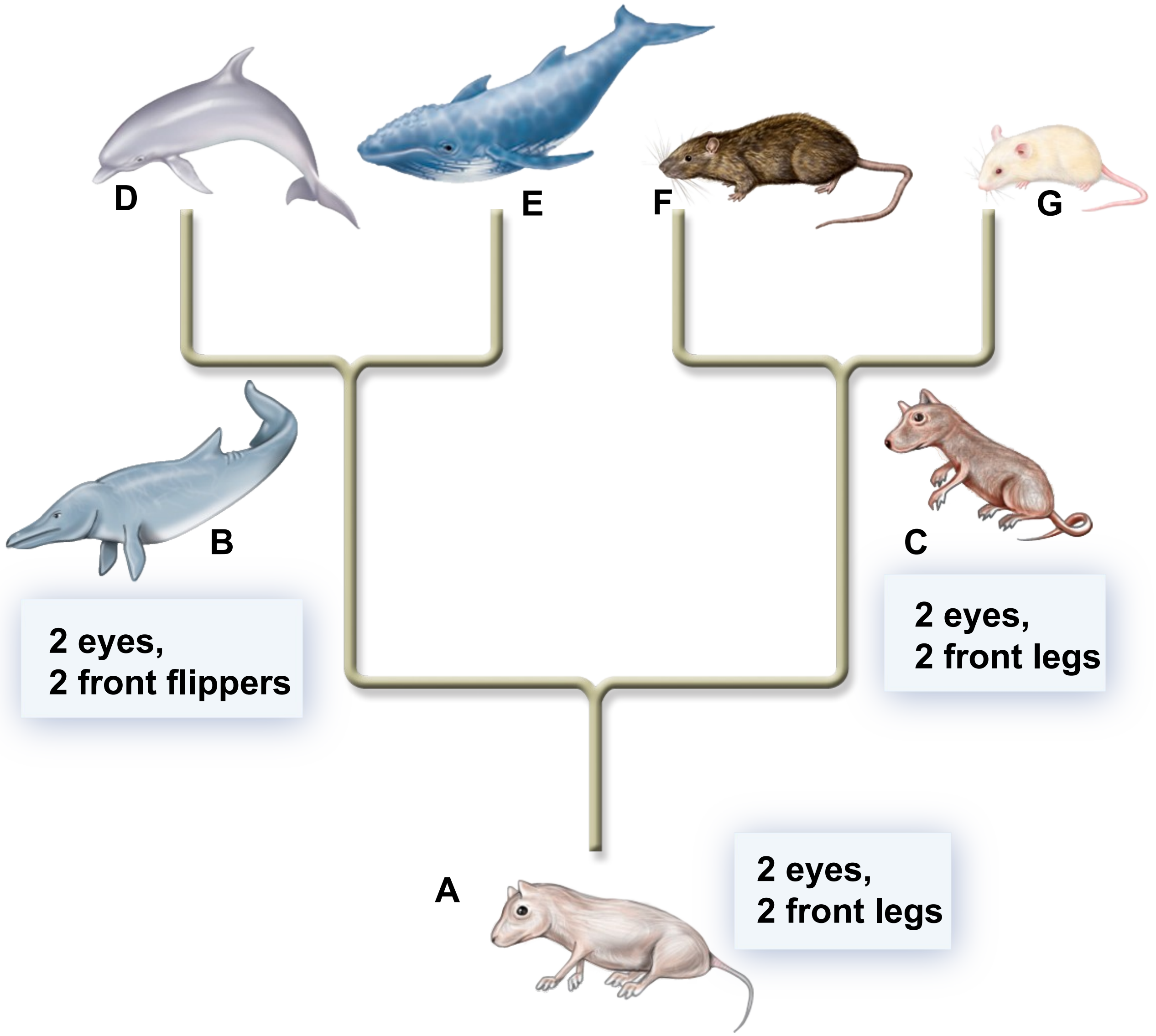


With regard to species D and E,

1. Shared derived character(s)

____

A. Eyes
B. Flippers
C. Backbone

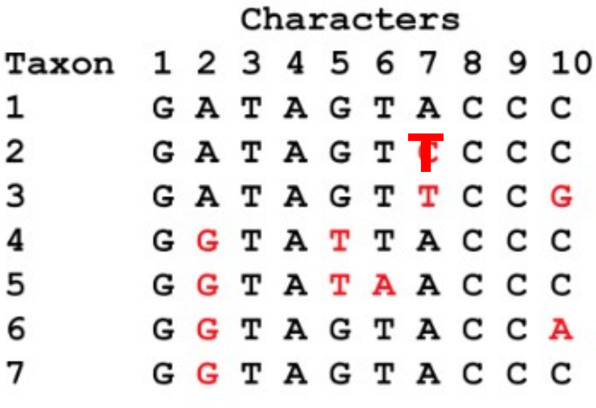


Principle of parsimony (maximum parsimony)

- Preferred hypothesis is the one that is the **simplest** for all the characters and their states
- **An hypothesis of relationships that requires the smallest number of character changes (smallest # of DNA mutations) is parsimonious**.
- Challenge in a cladistic approach is to determine the correct **order of events**
  - It may not always be obvious which traits are primitive (came earlier) and which are derived (came later in evolution)

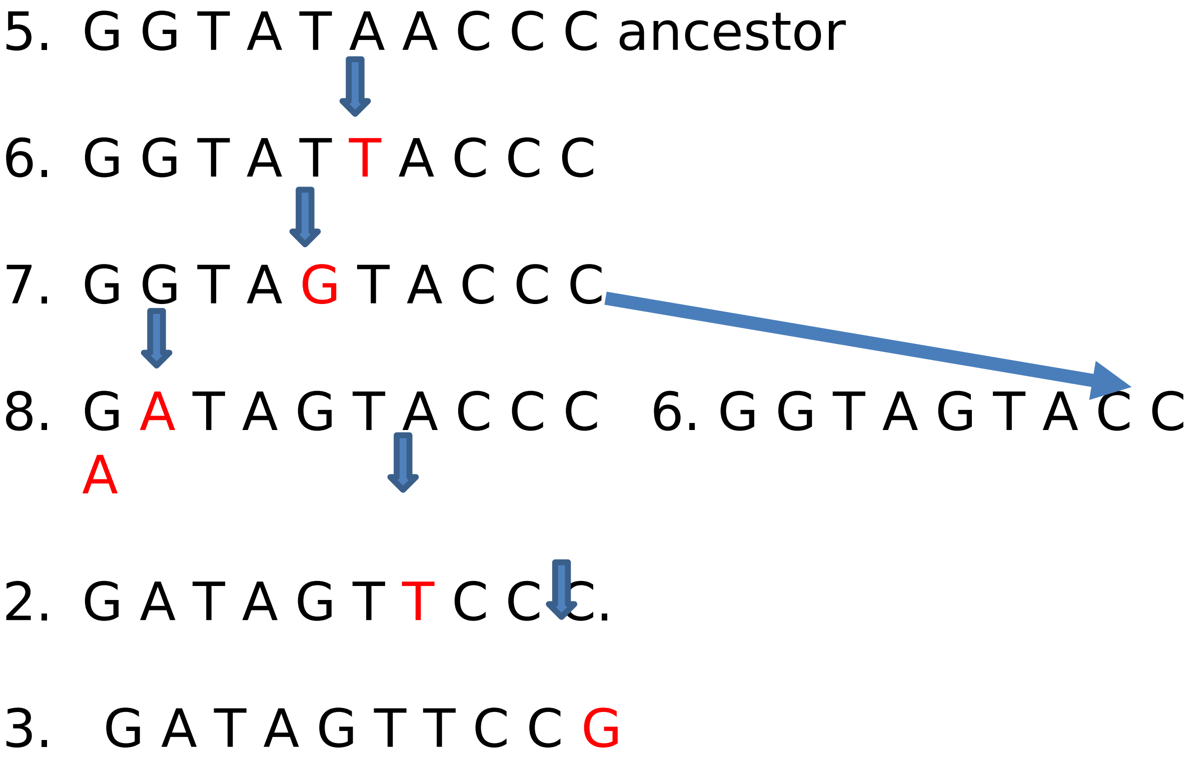
- A cladogram can also be constructed with gene sequences
- E.g. 7 species (TAXA) called 1-7
- A mutation that changes the DNA sequence is analogous to a change of a characteristic

	Characters									
Taxon	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	G	A	T	A	G	T	A	C	C	C
2	G	A	T	A	G	T	C	C	C	C
3	G	A	T	A	G	T	T	C	C	G
4	G	G	T	A	T	T	A	C	C	C
5	G	G	T	A	T	A	A	C	C	C
6	G	G	T	A	G	T	A	C	C	A
7	G	G	T	A	G	T	A	C	C	C



Taxon	1	2	3	4	5	6	7	8	9	10
						Characters				
1	G	A	T	A	G	T	A	C	C	C
2	G	A	T	A	G	T	T	C	C	C
3	G	A	T	A	G	T	T	C	C	G
4	G	G	T	A	T	T	A	C	C	C
5	G	G	T	A	T	A	A	C	C	C
6	G	G	T	A	G	T	A	C	C	A
7	G	G	T	A	G	T	A	C	C	C

Cladogram constructed with most parsimonious evolutionary order.



5. G G T A T A A C C C ancestor

6. G G T A T T A C C C

7. G G T A G T A C C C

8. G A T A G T A C C C   6. G G T A G T A C C C
A

2. G A T A G T T C C C.

3. G A T A G T T C C G

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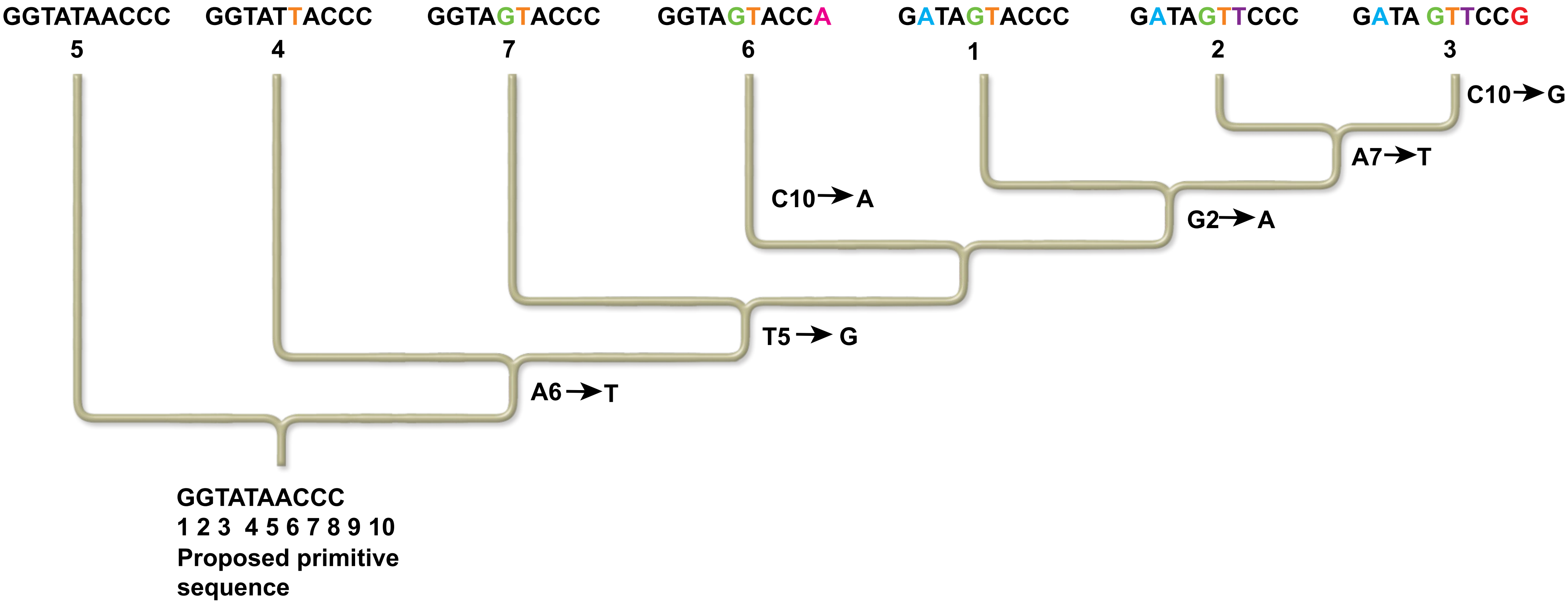


GGTATAACCC 5

GGTATTACCC 4

GGTAGTACCC 7

GGTAGTACCA 6

GATAGTACCC 1

GATAGTTCCC 2

GATA GTTCCG 3

C10 → G

A7 → T

C10 → A

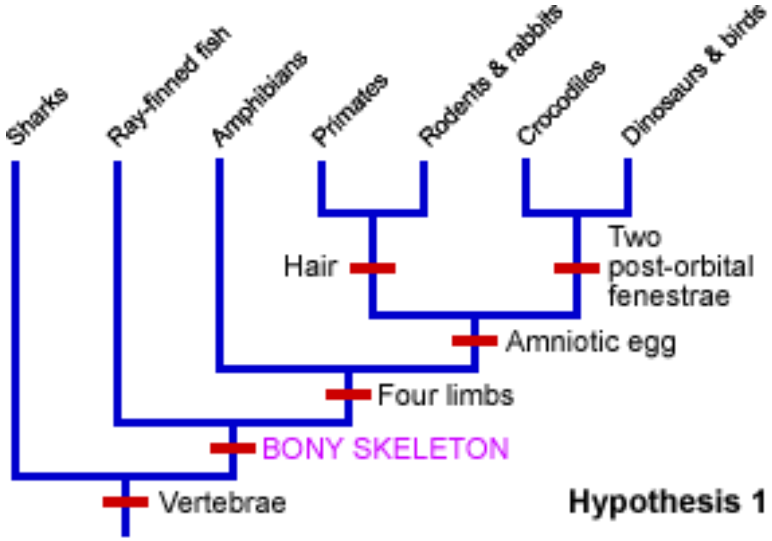
G2 → A

T5 → G

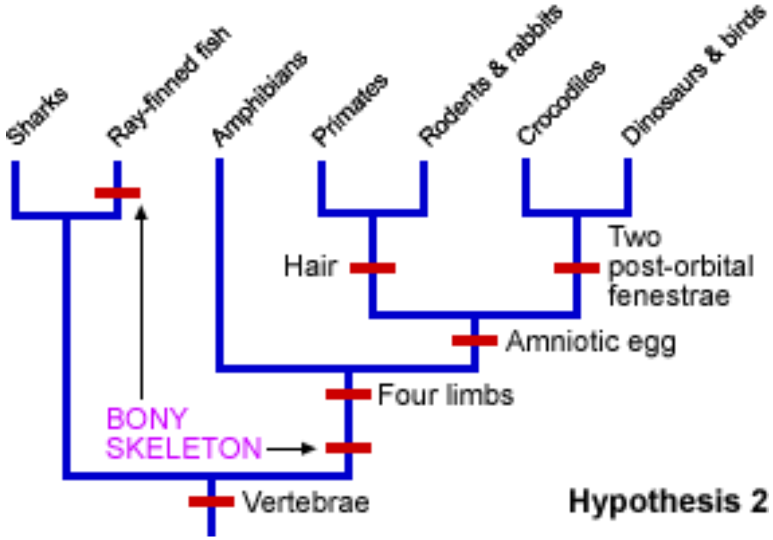
A6 → T

GGTATAACCC
1 2 3 4 5 6 7 8 9 10
Proposed primitive sequence

Which is the most parsimonious tree?



Hypothesis 1



Hypothesis 2

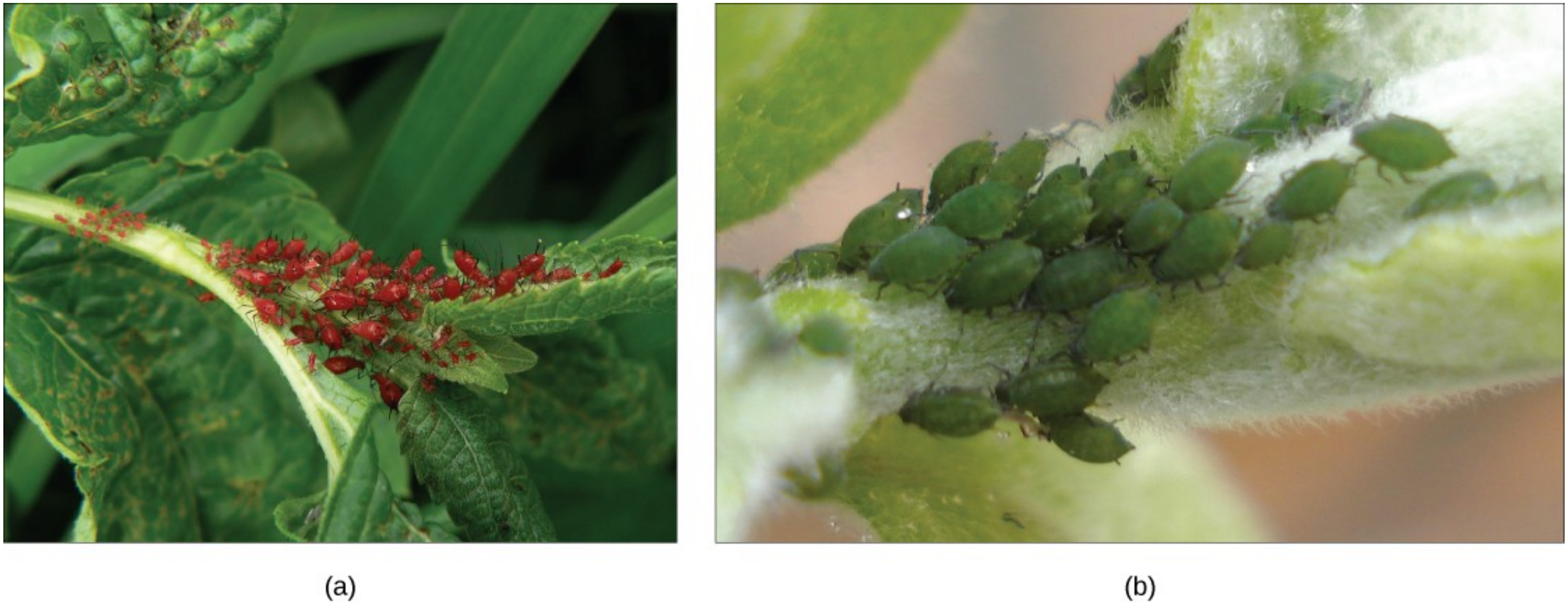
Horizontal Gene Transfer

- Any process in which an organism incorporates genetic material from another organism without being the offspring of that organism
- Vertical evolution (what we've already discussed)
  - Changes in groups due to **descent** from a common ancestor

Summary of Mechanisms of Prokaryotic and Eukaryotic Horizontal Gene Transfer HGT

	Mechanism	**Mode of Transmission**	**Example**
Prokaryotes	Transformation	DNA uptake	Prokaryotes (common)
	Transduction	Bacteriophage (virus)	Bacteria
	Conjugation	Pilus	Prokaryotes (common)
	Gene transfer agents GTAs	Phage-like particles	Purple non-sulfur bacteria 1st demonstrated
Eukaryotes	From food organisms	Unknown	Aphid eating fungus acquire gene for making carotenoids
	jumping genes	Transposons	Rice and millet
	Epiphytes/ parasites	Unknown	Yew tree fungi feeding on yew trees acquire genes for making taxol
	From viral infections		

Figure 20.13

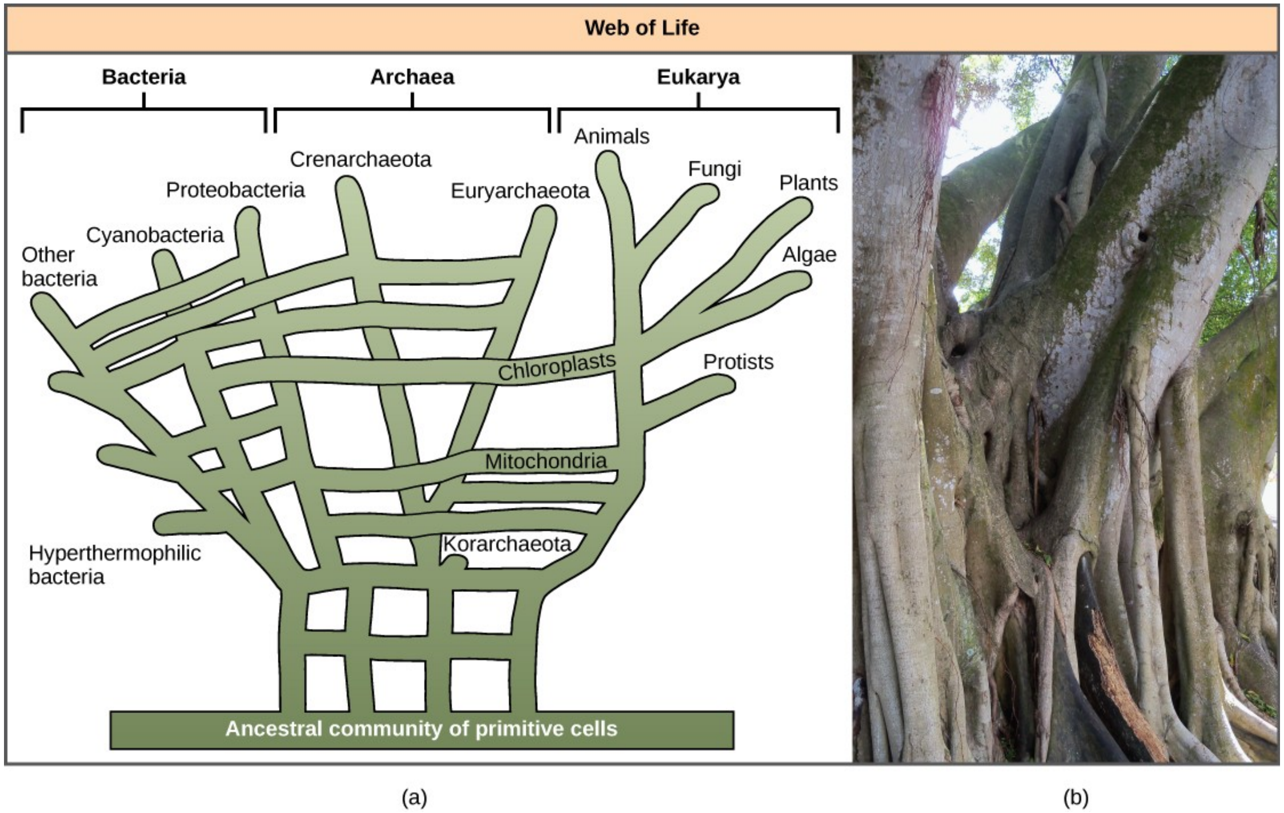


- (a) Red aphids get their color from red carotenoid pigment. Genes necessary to make this pigment are present in certain fungi, and scientists speculate that aphids acquired these genes through HGT after consuming fungi for food. If genes for making carotenoids are inactivated by mutation, the aphids revert back to (b) their green color. Red coloration makes the aphids a lot more conspicuous to predators, but evidence suggests that red aphids are more resistant to insecticides than green ones. Thus, red aphids may be more fit to survive in some environments than green ones. (credit a: modification of work by Benny Mazur; credit b: modification of work by Mick Talbot)

Due to Horizontal Gene Transfer, the Tree of Life Is Really a “Web of Life”

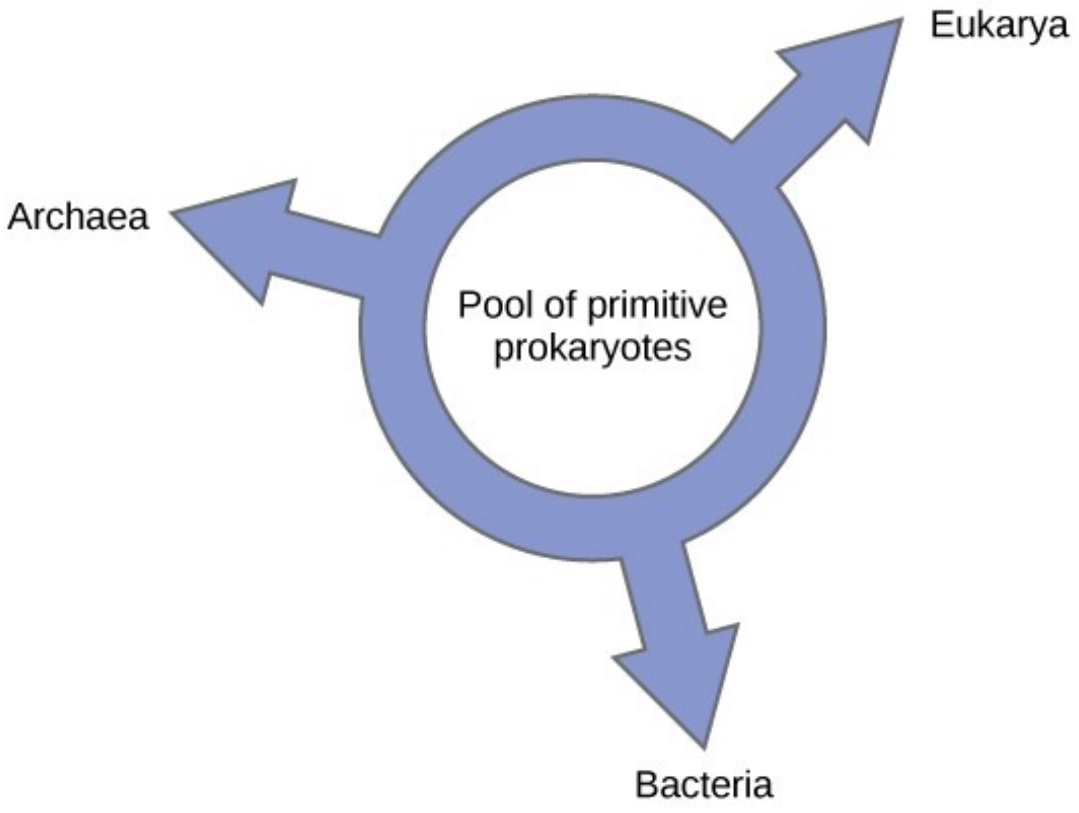
- Horizontal gene transfer is the transfer of genes between different species
- Significant role in phylogeny of **all living species**
- Still prevalent among prokaryotes but less common in eukaryotes
- Horizontal gene transfer may have been so prevalent that the universal ancestor may have been a **community of cell lineages**

Figure 20.16



- In the (a) phylogenetic model proposed by W. Ford Doolittle, the “tree of life” arose from a community of ancestral cells, has multiple trunks, and has connections between branches where horizontal gene transfer has occurred. Visually, this concept is better represented by (b) the multi-trunked **Ficus** than by the single trunk of the oak similar to the tree drawn by Darwin Figure 20.12. (credit b: modification of work by “psyberartist”/Flickr)

Figure 20.17



- According to the “ring of life” phylogenetic model, the three domains of life evolved from a pool of primitive gene-swapping prokaryotes.

If 36% of an African population is born with a severe form of sickle-cell anemia (ss), what percentage of the population will be more resistant to malaria because they are heterozygous(Ss) for the sickle-cell gene?

Show your work. You are solving for Genotype frequency of the heterozygote.

0.36 genotype frequency

Allele frequency (s) = square root of 0.36 = 0.6 =q

p+q=1. p=0.4

2pq = 2x0.4x0.6 = 0.48

SS frequency = 0.16

0.16 + 0.48 + 0.36 = 1